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incl. intef. !

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MPSRCH\_PP  
\*\*\*\*\* (TM)  
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Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Mon Feb 5 16:58:40 1996; MasPar time 4.63 Seconds  
Tabular output not generated. 343.730 Million cell updates/sec

Title: >FIG2  
Description: (1:220) from trans.pep  
Perfect Score: 1643  
Sequence: 1 MGAAARTIRLALGILLATL.....CAWYRGAPPKQEFIDIEP 220

Scoring table: PAM 150  
Gap 11

Searched: 62355 seqs, 7230759 residues

Database: a-geneseq20  
1 part1  
2 part2  
3 part3  
4 part4  
5 part5  
6 part6  
7 part7  
8 part8  
9 part9  
10 part10  
11 part11  
12 part12

Statistics: Mean 32.075; Variance 120.092; scale 0.267  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1643	100.0	220	12	R62769 Human metalloproteinase	1.02e-170
2	1643	100.0	220	2	R07955 Human metalloproteinase	1.02e-170

3	1550	94.3	220	2	R07954	Bovine metalloproteinase	4.04e-160
4	1550	94.3	220	12	R62769	Bovine metalloproteinase	4.04e-160
5	1554	88.5	194	2	R06898	Complete sequence of	3.40e-149
6	1396	85.0	186	2	R06898	Part of TIMP-2 metallo	1.34e-142
7	1377	83.8	192	2	R06895	Metalloproteinase inh	1.93e-140
8	1337	81.4	177	2	R06897	Part of TIMP-2 metallo	6.73e-136
9	521	31.7	207	3	P60786	Sequence of tissue in	2.50e-44
10	521	31.7	207	3	P60786	Sequence of human nat	2.50e-44
11	521	31.7	207	3	P60786	Sequence of a human p	2.50e-44
12	516	31.4	207	3	P60592	Sequence of a gibbon	8.83e-44
13	323	19.7	48	2	P60749	Peptide #1 for detect	6.44e-23
14	219	13.3	28	9	R47010	Metalloproteinase inh	4.12e-12
15	170	10.3	24	2	R06894	Peptide #3 for detect	3.05e-07
16	157	9.6	19	9	R47011	Metalloproteinase inh	5.46e-06
17	149	9.1	22	2	R10001	N-terminal sequence o	3.15e-05
18	147	8.9	47	3	P60276	N-terminal sequence o	4.87e-05
19	140	8.5	18	2	R06747	Immunogenic TIMP-2 pe	2.21e-04
20	139	8.3	23	2	R06750	Peptide #2 for detect	2.73e-04
21	137	8.3	18	2	R10002	Tryptic digestion pro	4.19e-04
22	130	7.9	16	2	R06748	Immunogenic TIMP-2 pe	1.85e-03
23	128	7.8	15	2	R10003	Tryptic digestion pro	2.82e-03
24	118	7.2	20	6	R31183	N-terminal of monocy	2.25e-02
25	117	7.1	15	2	R06746	Immunogenic TIMP-2 pe	2.77e-02
26	116	7.1	17	8	R42187	TIMP-2 peptide P-3.	3.40e-02
27	108	6.6	18	8	R42186	TIMP-2 peptide P-2.	1.71e-01
28	104	6.3	16	8	R42185	TIMP-2 peptide P-1.	3.79e-01
29	99	6.0	3033	6	R33214	NANBH virus strain HC	1.01e+00
30	93	5.7	383	10	R56166	Neuroendocrine tumor	3.20e+00
31	91	5.5	3033	6	R33539	NANBH virus strain HC	4.67e+00
32	88	5.4	385	10	R56167	Neuroendocrine tumor	8.18e+00
33	84	5.1	389	6	R29904	HCV NS4-NS5 peptide O	1.71e+01
34	84	5.1	365	7	R38287	NANBH hepatitis virus	1.71e+01
35	82	5.0	188	9	R53358	Hyalophora cecropia a	2.45e+01
36	82	5.0	188	1	P80507	Attacin.	2.45e+01
37	82	5.0	188	9	R53347	Hyalophora cecropia a	2.45e+01
38	80	4.9	389	6	R29876	HCV NS4-NS5 O30.	3.51e+01
39	80	4.9	318	12	R64174	Adhesion protein supp	3.51e+01
40	80	4.9	730	1	P80618	Human Bone Morphogeni	3.51e+01
41	79	4.8	389	6	R29905	HCV NS4-NS5 peptide O	4.19e+01
42	79	4.8	1411	6	R29533	HCV NS4-NS5 peptide I	4.19e+01
43	79	4.8	389	6	R29906	HCV NS4-NS5 peptide O	4.19e+01
44	79	4.8	1013	12	R62535	P. vulgaris chondroit	4.19e+01
45	79	4.8	323	1	R05711	Tumour-associated ant	4.19e+01

ALIGNMENTS

RESULT 1  
ID R62769 standard; Protein; 220 AA.  
AC R62769;  
DT 13-JUL-1995 (first entry)  
DE Human metalloproteinase inhibitor.  
KW Metalloproteinase inhibitor; tumour cell dissemination;  
KW rheumatoid arthritis; dystrophic epidermolysis bullosa;  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..26  
PN /label= sig\_peptide  
EP-623676-A.

P	encoding them, for treatment of tumour cell dissemination and
P	rheumatoid arthritis
P	Claim 12; Fig 2; 63pp; English.
P	The product has therapeutic use in inhibiting tumour dissemination
C	during chemotherapy and radiation therapy, impurged bone marrow cell
C	harvesting etc. The inhibitor may also be useful in encapsulating
C	harvesting etc. The inhibitor may also be useful in encapsulating
C	tumours aiding clean excision, and in treatment of enphysema, Paget's
C	disease, osteoporosis, scleroderma and bedsores.
C	The gene product also has application in autoimmune disorders eg.
C	rheumatoid arthritis and multiple sclerosis.
C	See also Q06583
S	Sequence 220 AA;
DB 2; Score 1643; Match 100.0%; QryMatch 100.0%; Pred. No. 1.02e-170;	
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	1 mgaartlrlalglalllatllrpdsacspvhpqgafcnadvvirakavsekevdsnd 60
Qy	1 MGAARTLRLALGLALLLATLLRPADACSCSFVHPQQAFCNADVIRAKAVSEKEVDSGND 60
Db	61 lygnpikriqyeikqimfkpekdieflytapasavcgvslvggkkeyliagkaegdg 120
Qy	61 IYGNPIKRIQYEIQRIMFKPEKDIEFIYAPASAVCGVSLDVGGRKEYLIAGKAEGDG 120
Db	121 kmhticdfivpwtlstqtqkkslnhryqmgceckitrcpmipcyissdecplwmdwvte 180
Qy	121 KMHTLCDFIVPWTLSLTQKKSINHRYQMGCECKITRCPMIPCYISSDECLWMDWVTE 180
Db	181 kninghqakffackirsdgscawyrgaapbkqefldiedp 220
Qy	181 KNINGHQAKFFACIKRSDGSCAWYRGAAPBKQEFLDIEDP 220
RESULT 3	
ID	R07954 standard; protein; 220 AA.
AC	R07954;
DE	21-FEB-1991 (first entry)
DE	Bovine metalloproteinase inhibitor gene product.
KW	Tumour; chemotherapy; cancer; Paget's disease; osteoporosis;
KW	scleroderma; cholesteatoma.
OS	Bos taurus.
FF	Key Location/Qualifiers
FT	Protein 27..220
FN	EP-398753-A.
PD	22-NOV-1990.
PF	18-MAY-1990; 305433.
PR	19-MAY-1989; US-355027.
PR	29-MAR-1990; US-501904.
PA	(AMGE-) AMGEN INC.
PA	(CHIL-) CHILDREN'S HOSPITAL OF LA.
PI	Langley KE, Boone TC, DeClerck YA;
DR	WPI; 90-350481/47.
DR	N-PSDB; Q06583.
P	New metallo-proteinase inhibitor polypeptide(s) - and DNA
P	encoding them, for treatment of tumour cell dissemination and
P	rheumatoid arthritis
P	Claim 12; Fig 1; 63pp; English.
C	The product has therapeutic use in inhibiting tumour dissemination
C	during chemotherapy and radiation therapy, impurged bone marrow cell
C	harvesting etc. The inhibitor may also be useful in encapsulating
C	harvesting etc. The inhibitor may also be useful in encapsulating

CC tumours aiding clean excision, and in treatment of enphysema, Paget's  
 CC disease, osteoporosis, scleroderma and bedsores.  
 CC The gene product also has application in autoimmune disorders eg.  
 CC rheumatoid arthritis and multiple sclerosis.  
 CC See also Q06584.  
 SQ Sequence 220 AA;

DB 2; Score 1550; Match 91.8%; QryMatch 94.3%; Pred. No. 4.04e-160;  
 Matches 202; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Db 1 mgaarslplafcllllgtllpradacscspvhpqafcnadivirakavnkkevsgnd 60  
 Qy 1 MGAARTLRALGELLATLLRPADACSCSPVHPQQAFCNADVIRAKAVSEKEVDSND 60

Db 61 iynpikriqyeikqimfkpgdqdiefiytapaavcgvsldigkkeyliagkaegng 120  
 Qy 61 IYGNPIKRIQYEIKQIMFKGPEKDIEFIYTAPSAVCGVSLDVGKKEYLIAGKAEGDG 120

Db 121 nmhitcdfiwpdttlsatqkkslnhrygmgeckitrcpmipcyisspdeclmwdvte 180  
 Qy 121 KMHITLDCFIWPDTTLSATQKKS LNHR YQMGECKITRCPMIPCYISSPDECLMWDWTE 180

Db 181 kninghqakffaciakrsdscawyrqgaappkqefliedp 220  
 Qy 181 KNINGHQAKFFACIKRS DSCAWYRG AAPPKQEF LIDEDP 220

RESULT 4  
 ID R62768 standard; Protein; 220 AA.  
 AC R62768;  
 DT 13-JUL-1995 (first entry)  
 DE Bovine metalloproteinase inhibitor  
 KW Metalloproteinase inhibitor; tumour cell dissemination;  
 KW rheumatoid arthritis; dystrophic epidermolysis bullosa;  
 KW enphysema; osteoporosis; MI gene disorders.  
 OS Bos taurus.  
 FH Key Location/Qualifiers  
 FT Peptide 1..26  
 FT /label= sig peptide  
 PN EP-623676-A.  
 PD 09-NOV-1994.  
 PF 18-MAY-1990; 305433.  
 PR 19-MAY-1989; US-355027.  
 PR 29-MAR-1990; US-501904.  
 PA (AMGE-) AMGEN INC.  
 PA (CHIL-) CHILDRENS HOSPITAL LOS ANGELES.  
 PI Boone TC, Declerck YA, Langley KE;  
 DR WPI; 94-343309/43.  
 DR N-PSDB; Q73087.  
 PT New metalloproteinase inhibitor, analogues and DNA - for  
 PT treating tumour cell dissemination, rheumatoid arthritis and for  
 PT large-scale recombinant inhibitor prodn.  
 PS Claim 12; Fig 1; 65pp; English.  
 CC Q73087 encodes R62768 bovine metalloproteinase inhibitor (MI), it  
 CC may be used to inhibit tumour cell dissemination and for treating  
 CC rheumatoid arthritis, dystrophic epidermolysis bullosa, emphysema  
 CC and osteoporosis. The DNA may be used to detect MI gene disorders.  
 SQ Sequence 220 AA;

DB 12; Score 1550; Match 91.8%; QryMatch 94.3%; Pred. No. 4.04e-160;

Matches 202; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Db 1 mgaarslplafcllllgtllpradacscspvhpqafcnadivirakavnkkevsgnd 60  
 Qy 1 MGAARTLRALGELLATLLRPADACSCSPVHPQQAFCNADVIRAKAVSEKEVDSND 60

Db 61 iynpikriqyeikqimfkpgdqdiefiytapaavcgvsldigkkeyliagkaegng 120  
 Qy 61 IYGNPIKRIQYEIKQIMFKGPEKDIEFIYTAPSAVCGVSLDVGKKEYLIAGKAEGDG 120

Db 121 nmhitcdfiwpdttlsatqkkslnhrygmgeckitrcpmipcyisspdeclmwdvte 180  
 Qy 121 KMHITLDCFIWPDTTLSATQKKS LNHR YQMGECKITRCPMIPCYISSPDECLMWDWTE 180

Db 181 kninghqakffaciakrsdscawyrqgaappkqefliedp 220  
 Qy 181 KNINGHQAKFFACIKRS DSCAWYRG AAPPKQEF LIDEDP 220

RESULT 5  
 ID R06898 standard; protein; 194 AA.  
 AC R06898;  
 DT 16-JAN-1991 (first entry)  
 DE Complete sequence of human TIMP-2 from clone pSS38.  
 KW matrix metalloproteinase inhibitor; TIMP-2; pSS38.  
 OS Synthetic.  
 PN US7494796-A.  
 PD 21-AUG-1990.  
 PF 13-MAR-1990; 494796.  
 PR 17-MAR-1989; US-326334.  
 PR 17-JUL-1989; US-380431.  
 PR 18-AUG-1989; US-395453.  
 PR 13-MAR-1990; US-494796.  
 PA (USSH ) NAT INST OF HEALTH.  
 PI Stetler-Sevenson WG, Liotta LA, Krutzsch HC;  
 DR WPI; 90-290097/38.  
 DR N-PSDB; Q05940.  
 PT New matrix metallo-proteinase inhibitor - used to treat diseases  
 PT resulting from matrix metallo-proteinase activity and in  
 PT diagnosis, detection and purificn..  
 PS Disclosure; Fig 7; 54pp; English.  
 CC TIMP-2 was isolated from human melanoma cell-conditioned media and  
 CC the amino acid sequence determined. A probe was synthesised  
 CC based upon the protein sequence information. It was used to screen  
 CC a LambdaGem-4 cDNA library prepared from human melanoma cells. 239  
 CC positives were identified from a total of 750,000 plaques screened.  
 CC Further analysis and screening with additional probes eliminated  
 CC most of the clones. Clone pSS38 was isolated and the nucleotide  
 CC sequence of the cDNA insert was determined. The deduced amino acid  
 CC sequence showed excellent agreement with that derived by directly  
 CC sequencing the TIMP-2 protein.  
 CC See also Q05937, R06746-R06750, R06894-R06895 and Q05938-Q05939.  
 SQ Sequence 194 AA;

DB 2; Score 1454; Match 99.5%; QryMatch 88.5%; Pred. No. 3.40e-149;  
 Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 cscapvhpqafcnadivirakavsekevsgndiynpikriqyeikqimfkpgkedi 60  
 Qy 27 CSCSPVHPQQAFCNADVIRAKAVSEKEVSGNDIYNPIKRIQYEIKQIMFKGPEKDI 86

```
Db 61 eflytapsavcqvslvvgkkeyliagkaegdkmhitlclcdfvpwdtltsttkkslnh 120
QY 87 EFYITAPSAVCGVSLVVGKKEYLIAGKAEGDKMHTLCLDFIVPMDTLSTTKKSLNH 146
Db 121 rymgceckitrcpmipcyisspdeclwmdwvtekninhgqakffacikrsgdscawyr 180
QY 147 RYQMGCECKITRCPMIPCYISSPDECLWMDWVTEKNINHQAQKFFACIKRSGDSCAWYR 206
Db 181 aappkqefldiedp 194
QY 207 AAPPKQEFLDIEDP 220

RESULT 6
ID R06896 standard; protein; 186 AA.
AC R06896;
DT 16-JAN-1991 (first entry)
DE Part of TIMP-2 metalloproteinase inhibitor, encoded by clone pSS15.
KW matrix metalloproteinase inhibitor; TIMP-2; pSS15.
OS Synthetic.
PN US7494796-A.
PD 21-AUG-1990.
PF 13-MAR-1990; 494796.
PR 21-MAR-1989; US-326334.
PR 17-JUL-1989; US-380431.
PR 18-AUG-1989; US-395453.
PR 13-MAR-1990; US-494796.
PA (USSH ) NAT INST OF HEALTH.
PI Stetler-Sevenson WG, Liotta LA, Krutzsch HC;
DR WPI; 90-290097/38.
DR N-PSDB; Q05938.
PT New matrix metallo-proteinase inhibitor - used to treat diseases
PT resulting from matrix metallo-proteinase activity and in
PT diagnosis, detection and purificn..
PS Disclosure; Fig 8A; 54pp; English.
CC TIMP-2 was isolated from human melanoma cell-conditioned media and
CC the amino acid sequence determined. A probe was synthesised
CC based upon the protein sequence information. It was used to screen
CC a LambdaGen-4 cDNA library prepared from human melanoma cells. 239
CC positives were identified from a total of 750,000 plaques screened.
CC Further analysis and screening with additional probes eliminated
CC all but two clones (pSS15 and pSS18). Both were sequenced and found
CC to encode CSC-21K (=TIMP-2), a novel metalloproteinase inhibitor.
CC This is the amino acid sequence deduced from the cDNA sequence of
CC pSS15.
CC See also Q05937, R06746-R06750, R06894-R06895 and Q05939-Q05940.
SQ Sequence 186 AA;

DB 2; Score 1396; Match 99.5%; QryMatch 85.0%; Pred. No. 1.34e-142;
Matches 185; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 qqafcnadvirakavnskevsgndiynpikriqyeikqkfkfgekiefiytaps 60
QY 35 QQAFCNADVIRAKAVNSKEVSGNDIYNPIKRIQYEIKQKFKFGEKDI EYITAPS 94
Db 61 savcgvslvvgkkeyliagkaegdkmhitlclcdfvpwdtltsttkkslnhrymgcec 120
QY 95 SAVCGVSLVVGKKEYLIAGKAEGDKMHTLCLDFIVPMDTLSTTKKSLNHRHYMGCEC 154
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Db 121 kitrcpmipcyisspdeclwmdwvtekninhgqakffacikrsgdscawyr 180
QY 155 KITRCPMIPCYISSPDECLWMDWVTEKNINHQAQKFFACIKRSGDSCAWYRGAAPPKQEF 214
Db 181 ldiedp 186
QY 215 LDIEDP 220

RESULT 7
ID R06895 standard; protein; 192 AA.
AC R06895;
DT 16-JAN-1991 (first entry)
DE Metalloproteinase inhibitor TIMP-2.
KW matrix metalloproteinase inhibitor; TIMP-2 (CSC-21K).
OS Synthetic.
PN US7494796-A.
PD 21-AUG-1990.
PF 13-MAR-1990; 494796.
PR 21-MAR-1989; US-326334.
PR 17-JUL-1989; US-380431.
PR 18-AUG-1989; US-395453.
PR 13-MAR-1990; US-494796.
PA (USSH ) NAT INST OF HEALTH.
PI Stetler-Sevenson WG, Liotta LA, Krutzsch HC;
DR WPI; 90-290097/38.
PT New matrix metallo-proteinase inhibitor - used to treat diseases
PT resulting from matrix metallo-proteinase activity and in
PT diagnosis, detection and purificn..
PS Disclosure; Fig 5; 54pp; English.
CC Protein was isolated from human melanoma cell-conditioned media by
CC gelatin-affinity chromatography.
CC It inhibits matrix metalloproteinases and can be used to treat
CC diseases such as arthritis, diabetes, cancer, ulcers of mucosa and
CC epithelial tissues, autoimmune-mediated inflammation, lung injury,
CC granulomatous diseases and myocardial infarctions. It can also be
CC used as a birth control agent by preventing embryo/placental
CC attachment or invasion. Other therapeutic benefits may also be
CC obtd. in diseases with basement destruction or myocyte destruction.
CC See also Q05937, R06746-R06750, R06894 and Q05938-Q05940.
SQ Sequence 192 AA;

DB 2; Score 1377; Match 96.4%; QryMatch 83.8%; Pred. No. 1.93e-140;
Matches 186; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Db 1 cscapvhpqgafcnadvirakavnskevsgndiynpikriqyeikqkfkfgekdi 60
QY 27 CSCAPVHPQGAFCNADVIRAKAVNSKEVSGNDIYNPIKRIQYEIKQKFKFGEKDI 86
Db 61 eflytapsavcgvslvvgkkeyliagkae-dgkrrhitclcdfvpwdtltsttkkslnh 119
QY 87 EFYITAPSAVCGVSLVVGKKEYLIAGKAEGDKMHTLCLDFIVPMDTLSTTKKSLNH 146
Db 120 rymgceckitrcpmipcyisspdeclwtdwvtekninhgqakffacikrsgdscawyr 179
QY 147 RYQMGCECKITRCPMIPCYISSPDECLWMDWVTEKNINHQAQKFFACIKRSGDSCAWYR 206
Db 180 aappkqefldied 192
QY 207 AAPPKQEFLDIED 219
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**Listing for Mary Hale**

FH	Key	Location/Qualifiers
FT	Peptide	1..23
FT	/label= signal	
FT	Protein	
FT	Modified -site	24..207
FT	Modified -site	53..55
FT	/label= potential N-glycosylation site	
FT	Modified -site	101..103
FT	/label= as above	
PN	GB2169295-A.	
PD	09-JUL-1986.	
PF	06-JAN-1986;	000199.
PF	05-OCT-1983;	BE-897924.
PR	07-JAN-1985;	GB-000341.
PR	07-JAN-1985;	GB-500341.
PR	01-NOV-1985;	GB-026951.
PR	06-JAN-1986;	GB-000199.
PA	(CELL-) CELTECH LTD.	
PI	Harris TJR, Reynolds JJ, Docherty AJP,	
DR	WFI; 86-177873/28.	
DR	N-PSDB; N60538.	
PT	Prodn. of metallo-proteinase inhibitor	
PT	techniques	
PS	Disclosure; Fig 3; 16pp; English.	
PS	A gene with residues 64-684 of N60538	
CC	Isolated from human a foetal diploid l	
CC	library using N60539.	
SC	Sequence	207 AA;
DB	3; Score	521; Match 41.1%; Qryv
	Matches	81; Conservative 39; Mismat
Db	7 laaglllllwlialpractcvpphptafcn	
Qy	10 LALGLLILLATLTPKADACSCSPVHPQQAF	
Db	66 tk-mvkgfcal-gdaadirfvytpameavc	
Qy	69 IQEIKQIKMFKGPKEDIEFYTPAPSSAV	
Db	123 sfvawpwnslaqrfgrtktytvgceetvfp	
Qy	128 DFIVPMDTLSTOKKSILNHRVQMGE-C	
Db	183 qsrhlacilpreplgtw 199	
Qy	187 QAKFFACIKRSDGSCAW 203	
RESULT 10		
ID	P60275 standard; Protein; 207 AA.	
AC	P60275;	
DT	08-AUG-1991 (first entry)	
DE	Sequence of human natural inhibitor	
KW	Metallo-proteinase inhibitor; wound he	
KW	rheumatoid arthritis inhibitor; ulcerati	
FH	Key	Location/Qualifiers
FT	Peptide	1..23
FT	/label= signal	
FT	Protein	
FT	/note= "claimed"	24..207

RESULT	8	
ID	R06897	standard; protein; 177 AA.
AC	R06897;	
DE	16-JAN-1991	(first entry)
DT	Part of TIMP-2 metalloproteinase inhibitor,	encoded by clone pSS18.
DE	Part of TIMP-2 metalloproteinase inhibitor; TIMP-2;	pSS18.
KW	matrix metalloproteinase inhibitor;	
OS	Synthetic.	
PN	US7494796-A.	
PD	21-AUG-1990.	
PF	21-AUG-1990.	494796.
PR	13-MAR-1990;	US-326334.
PR	21-MAR-1989;	US-380431.
PR	17-JUL-1989;	US-380431.
PR	18-AUG-1989;	US-395453.
PR	13-MAR-1990;	US-494796.
PA	(USSH ) NAT INST OF HEALTH.	
PI	Stetler-Sevenson WG, Liotta LA, Krutzsch HC;	
PI	WPI: 90-290097/38.	
DR	N-PSDB; Q05939.	
PT	New matrix metallo-proteinase inhibitor - used to treat diseases	
PT	resulting from matrix metallo-proteinase activity and in	
PT	diagnosis, detection and purification..	
PT	Disclosure; Fig 6B; 54pp; English.	
CC	TIMP-2 was isolated from human melanoma cell-conditioned media and	
CC	the amino acid sequence determined. A probe was synthesised	
CC	based upon the protein sequence information. It was used to screen	
CC	a LambdaGem-4 cDNA library prepared from human melanoma cells. 239	
CC	positives were identified from a total of 750,000 plaques screened.	
CC	Further analysis and screening with additional probes eliminated	
CC	all but two clones (pSS15 and pSS18). Both were sequenced and found	
CC	to encode CSC-21K (=TIMP-2), a novel metalloproteinase inhibitor.	
CC	This is the amino acid sequence deduced from the cDNA sequence of	
CC	pSS18.	
CC	See also Q05937, R06746-R06750, R06894-R06895, Q05938 and Q05940.	
CC	Sequence 177 AA;	
CC		

DB 2; Score Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	1 virakavsekevdsgndiynvpikriqyeikqkmfkpekdiefiytapassavcgvsl 60       
Qy	44 VIRAKAVSEKVDSGNDIYGNP IKRIQYEIKQIKMFKPEKDIEFIYTPASSAVCGVSLD 103       
Db	61 vgakkeyliagkaegdkmhltcdfipwvdtlstkqkshnrygmgeckitrcmpip 120       
Qy	104 VGGKKEYLIAGKAEGDGKMHITLCDFI VPDWTLSTQKSHNRYGMGECKITRCMPIP 163       
Db	121 cyisrpdeclwmdwvteknghqakffacikrdsdcawyrqaapbkqefldiedp 177       
Qy	164 CYISRPDECLWMDWTERKNGHQAKFTACIKRSDGCAWYRGAAPBKQEFLDIEDP 220       

RESULT 9  
ID P60786 standard; Protein; 207 AA.  
AC P60786;  
DT 08-AUG-1991 (first entry)  
DE Sequence of tissue inhibitor of metalloproteinase (TIMP).  
KW Connective tissue; extracellular matrix.  
OS Homo sapiens.

**Tue Feb 6 11:36:52 1996**

FT	Modified -site 53...55	
FT	/note= "potential glycosylation site"	
FT	Modified -site 101..103	
FT	/note= "potential glycosylation site"	
PN	EP-189784-A.	
PD	06-AUG-1986.	
PD	16-JAN-1986; 100482.	
PR	18-JAN-1985; US-692808.	
PI	(SEAR ) SEARLE G D & CO.	
PI	Galloway WA, Clissold PM, McCullagh KG;	
WI	WPI; 86-205910/32.	
DR	N-PSDB; N60277.	
PT	New human natural inhibitor of collagenase - for treating e.g.	
PT	rheumatoid arthritis or ulceration, and new DNA sequences coding	
PT	for it	
PS	Disclosure; Fig 2; 51pp; English.	
CC	The patentors claim the AA SQ of human NIC, DNA sequences coding for	
CC	NIC, and its RNA analogues and plasmids contg. this DNA. NIC	
CC	inhibits the activity of metallo-proteinases, esp. of collagenase,	
CC	proteoglycanase, gelatinase or a leucocyte, macrophage or tumour	
CC	cell metallo-proteinase.	
SC	Sequence 207 AA;	
DB	3; Score 521; Match 41.1%; OryMatch 31.7%; Pred. No. 2.50e-44;	
Matches	81; Conservative 39; Mismatches 70; Indels 7; Gaps 7;	
Db	7 lasglllllwiapsractcpvphptafonsedlvirakfvgtpevnqtt-lyqryeikm 65	
Qy	10 LALGILLIATLIRPADACSPVHPQQAFCADVIRAKAVSEKVDSDNDIYGN-PIKR 68	
Db	66 tk-mvkgfqal-gdaadirfvtpamesvcvgvfhrrshnrseefliagklg-dgllhittc 122	
Qy	69 IQYEIKQIKMFKGPEKDIEFIYTAPSAVCGVSLDVGGKKE-ILTAGKAEGDGKMHITLC 127	
Db	123 sfvawpnalsiaqrgtfgtktyvtvgceetvfpclsipcklqgthclwtdqllgsekqf 182	
Qy	128 DRIVEPDTLSITQKSLNHRVQMGE-CKITRCMPICPVISSPEDECLMWDWTEKINGH 186	
Db	183 qsrhlaclprepglctw 199	
Qy	187 QAKFFACIKRSDGSCAW 203	
RESULT	11	
ID	P60592 standard; Protein; 207 AA.	
AC	P60592;	
DE	13-AUG-1991 (first entry)	
DT	Sequence of a human protein having erythroid potentiating	
DE	activity (EPA).	
OS	Erythroid precursor growth; anaemia therapy.	
KW	Homo sapiens.	
PN	W08602100-A.	
PD	10-APR-1986.	
PR	01-OCT-1985; 501900.	
PR	01-OCT-1984; US-656590.	
PA	(SANO ) SANDOZ LTD.	
PA	(REGC ) REGENTS OF UNIV OF CALIF.	
PI	Brown E, Clark S, Golde DW, Casson JC, Hewick R, Westbrook CA;	
WI	WPI; 86-106663/16.	
DR	N-PSDB; N60494.	

PT	Vectors contg. gene for protein having erythroid potentiating activity - used for producing protein to stimulate growth and formation of erythroid cells
PT	Disclosure; Fig 4; 59pp; English.
CC	The inventors claim human and gibbon EPA proteins (P60592, P60593) and cDNA that encodes EPA (N60494, N60495). The EPA protein has a biological activity of at least about 1,000,000 units per mg of protein and has an apparent molecular weight of about 28,000 daltons.
SQ	Sequence 207 AA;
DB	3; Score 521; Match 41.1%; QRYMatch 31.7%; Pred. No. 2.50e-44; Matches 81; Conservative 39; Mismatches 70; Indels 7; Gaps 7;
Dn	7 lasgillllwlisractevvpbphtafonsdlvirakfvgtpevngctt-lyqrvyeikm 65    : :    ::    : :         :      :   : ::     
Qy	10 LALGILLLLATLIRPADACSGSPVHPQQAFNCADVWIRAKAVSEKVEVDSCNDIYGN-PIKR 68     : :    ::    : :         :      :   : ::
Dn	66 tk-mykkgfqa -gdaadirfytpamesvcgyfhrehnrseefliaqklg-dglilhittc 122     : :    ::    : :    ::     ::    : :    ::     :
Qy	69 IQYEIKQRIMRFGEPEKDIEFYTPASSAGCVSLDVGGKKKE-YLIAGRAEGDGKRHHITLC 127     : :    ::    : :    ::     ::    : :    ::     :
Dn	123 sfvapwnsliaqrgrfktyvtvgceectvfpcslspkqlsgtgchclwtddlllgsekfg 182    : :    ::    : :    ::     ::    : :    ::     :
Qy	128 DFIVPWDLTISTQKSINHRXQMGCCE-CKITRCPIPCVISSPFDECLMWDVVTEKNINGH 186     : :    ::    : :    ::     ::    : :    ::     :
Dn	183 qerhlaciaprepplctw 199   :    :      :
Qy	187 QAKFACFKRSDDGSAAW 203   :    :      :
RESULT	12
ID	P60593 standard; Protein; 207 AA.
AC	P60593;
DT	13-AUG-1991 (first entry)
DE	Sequence of a gibbon protein having erythroid potentiating activity (EPA).
DE	Erythroid precursor growth; anaemia therapy.
KW	Gibbon.
OS	WO8602100-A.
PN	10-APR-1986.
PD	01-OCT-1985; 501900.
PR	01-OCT-1984; US-656590.
PA	(SANO ) SANDOZ LTD.
PA	(REGC ) REGENTS OF UNIV OF CALIFO.
PI	Brown E, Clark S, Golde DW, Casson JC, Hewick R, Westbrook CA; WFI: 86-106663/16. N-PSDIB; N60495.
DR	N-PSDIB; N60495.
PT	Vectors contg. gene for protein having erythroid potentiating activity - used for producing protein to stimulate growth and formation of erythroid cells
PT	Disclosure; Fig 5; 59pp; English.
CC	The inventors claim human and gibbon EPA proteins (P60592, P60593) and cDNA that encodes EPA (N60494, N60495). The EPA protein has a biological activity of at least about 1,000,000 units per mg of protein and has an apparent molecular weight of about 28,000 daltons.
CC	Sequence 207 AA;

DB 3; Score 516; Match 40.6%; QryMatch 31.4%; Pred. No. 8.83e-44;  
Matches 80; Conservative 40; Mismatches 70; Indels 7; Gaps 7;

Db	7	lasgllllllwliapsractcvphpqtafcansdlvikakfvgtpevnqtt-lyrryveikm	65
Qy	10	lalglllllaltllrpadacspvhpoqafcnadvvirakavsekevsgndiycn-pikr	68
Db	66	tk-mykafqal-gdaadirfvtpamesvcgyfhrshnrseefiakqlg-dqllhitt	122
Qy	69	lqyeikqlkmfkqpekdiefiytapsavcgvslvdvgkke-yliagkaegdgkmituc	127
Db	123	sfvapwnslslagrgftktytvgceectvfcpaispklsgthclwtqdllqgsekf	182
Qy	128	dfivpwtlsltkkslnhryqmgce-cklfrcpmipcyisspdeclawmdwvtekninh	186
Db	183	qsrhlacclprepqlctw	199
Qy	187	oaktfacikrsgdscaw	203

RESULT	13	
ID	R06749	standard; protein; 48 AA.
AC	R06749;	
DT	16-JAN-1991	(first entry)
DE	Peptide #1 for detection of metalloproteinases.	
DE	matrix metalloproteinase; TIMP-2 (CSC-21K).	
OS	Synthetic.	
PN	US7494796-A.	
PD	21-AUG-1990.	494796.
PF	13-MAR-1990;	PF
PP	21-MAR-1989;	US-328334.
PR	17-JUL-1989;	US-380431.
PR	18-AUG-1989;	US-395453.
PR	13-MAR-1990;	US-494796.
PR	(USSH ) NAT INST OF HEALTH.	
PPI	Stetler-Sevenson WG, Liotta LA, Krutzsch HC;	
DR	WPI; 90-290097/38.	
PPT	New matrix metallo-proteinase inhibitor - used to treat diseases	
PPT	resulting from matrix metallo-proteinase activity and in	
PPT	diagnosis, detection and purific..	
PPT	Example; Page 37; 54pp; English.	
CCC	One of three peptides lacking cysteine or having only one cysteine	
CCC	which were found to be useful for detecting metalloproteinases in	
CCC	animal and human tissues or in body fluids which may have	
CCC	antibodies to the protein. The peptides can also be used to elicit	
CCC	antibodies for use in detecting metalloproteinases.	
CCC	See also Q05937, R06746-R06748, R06750, R06894-R06895 and	
CC	Q05938-Q05940.	
CS	Sequence	48 AA;

DB 2; Score 323; Match 93.8%; QryMatch 19.7%; Pred. No. 6,44e-23;  
Matches 45; Conservative 1; Mismatches 2; Indels 0; Caps 0;

Db

1 diynpnkrqveikqkfkfgiekdiefiyrtapsavcgveldvgk 48  
|||||  
60 DIYGNPDKRQYIKQKFKFGPEKDIEFIYTAPSSAVCGVSLDVGK 107  
|||||

RESULT	14
ID	R47010 standard; Protein; 28 AA.
AC	R47010;
DT	16-SEP-1994 (first entry)
DE	Metalloproteinase inhibitor 2 position 187-214.

KKW	Naturally-occurring; immunomodulatory protein; human; therapy; class I;
KKW	major histocompatibility complex; class II; allotype; type I diabetes;
KKW	autoimmune disease; rheumatoid arthritis; T-cell-mediated response;
KKW	multiple sclerosis; transplant rejection; vaccine; MHC.
OS	Homo sapiens.
FPN	WO9404171-A.
FPD	03-MAR-1994.
FPF	11-AUG-1993; U07545.
PPF	11-AUG-1993; US-925460.
PPR	11-AUG-1992; US-925460.
PPS	15-JUN-1993; US-925460.
PPA	(HARD ) HARVARD COLLEGE.
PPB	Chicz RM, Hedley ML, Stern LJ, Strominger JL, Urban RG;
PPI	Vignali DA;
PPI	WPI; 94-082825/10.
PDR	Novel immunomodulatory peptide(s) and nucleic acids - useful for
PPT	treatment of auto:immune diseases, transplant rejection and for
PPT	vaccination
PPT	Disclosure; Page 48; 139pp; English.
PPS	The sequences given in R49291-505 and R46981-7038 represent peptide
CCC	fragments of naturally-occurring immunomodulatory proteins. These
CCC	fragments are between 10-30 residues in length and bind to a human
CCC	major histocompatibility complex (MHC) class II allotype. These
CCC	peptides may be used for therapy of autoimmune diseases, such as
CCC	type I diabetes, rheumatoid arthritis and multiple sclerosis, and to
CCC	reduce transplant rejection. They may also be used for vaccination
CCC	providing an exclusively T-cell-mediated response, which can be
CCC	class I or class-II based, or both, depending on the length and
CCC	character of the immunogenic peptides.
CSQ	Sequence 28 AA;

```
DB 9; Score 219; Match 100.0%; QryMatch 13.3%; Pred. No. 4.12e-12;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 qakffacikrdsdgcawyrgaappkqef 28
      |||||
QV 187 QAKFFACIKRSDGSCAWYRGAAPPKQEF 214
      |||||
```

RESULT 15  
 ID R06894 standard; protein; 24 AA.  
 AC R06894;  
 DDT 16-JAN-1991 (first entry)  
 DE Peptide #3 for detection of metalloproteinases.  
 KW matrix metalloproteinase; TIMP-2 (CSC-21K).

[illegible]

Example; Page 37; 34pp; English.  
One of three peptides lacking cysteine or having only one cysteine

CC which were found to be useful for detecting metalloproteinases in  
CC animal and human tissues or in body fluids which may have  
CC antibodies to the protein. The peptides can also be used to elicit  
CC antibodies for use in detecting metalloproteinases.  
CC See also Q05937, R06746-R06750, R06895 and Q05938-Q05940.  
SQ Sequence 24 AA;

DB 2; Score 170; Match 100.0%; QryMatch 10.3%; Pred. No. 3.05e-07;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 hitlclfdvfpwdtlsttqkksln 24

QY 123 HITLCLFDVFPWDTLSTTQKKSIN 145

Search completed: Mon Feb 5 16:59:06 1996  
Job time : 26 secs.

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WIPERH (TM)

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Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Feb 5 17:01:32 1996; MasPar time 2.09 Seconds  
194.539 Million cell updates/sec

Tabular output not generated.

Title: >FIG2  
Description: (1:220) from trans.pep  
Perfect Score: 1643  
Sequence: 1 MGAARTLRALGLLLATL.....CAWYRGAPPKQEFLLIEDP 220

Scoring table: PAM 150  
Gap 11

Searched: 19663 seqs, 1851369 residues

Database: a-issued

1 51  
2 52  
3 53  
4 54  
5 PCT90  
6 PCT91  
7 PCT92  
8 PCT93  
9 PCT94  
10 PCT95

Statistics: Mean 30.075; Variance 124.991; scale 0.241

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description	Pred. No.
1	219	13.3	28	8	PCT-US93-0 Sequence 245, Applicat	1.40e-11
2	157	9.6	19	8	PCT-US93-0 Sequence 246, Applicat	5.57e-06
3	91	5.5	3033	4	US-07-925-0 Sequence 9, Applicatio	1.68e+00
4	91	5.5	3033	4	US-07-925-0 Sequence 8, Applicatio	1.68e+00
5	79	4.8	990	10	PCT-US95-0 Sequence 2, Applicatio	1.32e+01
6	79	4.8	476	9	PCT-US94-0 Sequence 12, Applicati	1.32e+01
7	79	4.8	397	10	PCT-US95-0 Sequence 14, Applicati	1.32e+01
8	75	4.6	928	9	PCT-US94-1 Sequence 3, Applicatio	2.55e+01
9	75	4.6	928	9	PCT-US94-1 Sequence 3, Applicatio	2.55e+01
10	74	4.5	490	10	PCT-US95-0 Sequence 13, Applicati	3.00e+01
11	74	4.5	778	8	PCT-US93-0 Sequence 4, Applicatio	3.00e+01
12	74	4.5	480	4	US-07-803-0 Sequence 2, Applicatio	3.00e+01
13	73	4.4	883	3	US-08-106-0 Sequence 2, Applicatio	3.53e+01
14	71	4.3	659	10	PCT-US95-0 Sequence 8, Applicatio	4.86e+01
15	70	4.3	239	8	PCT-US93-0 Sequence 1, Applicatio	5.70e+01
16	70	4.3	2446	8	PCT-US93-1 Sequence 2, Applicatio	5.70e+01
17	70	4.3	1513	8	PCT-US93-0 Sequence 2, Applicatio	5.70e+01
18	70	4.3	778	8	PCT-US93-0 Sequence 3, Applicatio	5.70e+01
19	70	4.3	112	8	PCT-US93-0 Sequence 3, Applicatio	5.70e+01
20	69	4.2	104	3	US-07-789-0 Sequence 8, Applicatio	6.67e+01
21	69	4.2	180	4	US-07-953-0 Sequence 12, Applicati	6.67e+01
22	69	4.2	286	8	PCT-US93-0 Sequence 65, Applicati	6.67e+01
23	69	4.2	336	7	PCT-US92-1 Sequence 2, Applicatio	6.67e+01
24	68	4.1	474	10	PCT-US95-0 Sequence 5, Applicatio	7.80e+01
25	68	4.1	434	2	US-07-679-0 Sequence 15, Applicati	7.80e+01
26	68	4.1	567	4	US-08-007-0 Sequence 2, Applicatio	7.80e+01
27	68	4.1	214	4	US-07-953-0 Sequence 11, Applicati	7.80e+01
28	67	4.1	575	3	US-07-683-0 Sequence 2, Applicatio	7.80e+01
29	67	4.1	3011	9	PCT-US94-0 Sequence 1, Applicatio	9.12e+01
30	67	4.1	3011	10	PCT-US95-0 Sequence 1, Applicatio	9.12e+01
31	67	4.1	364	8	PCT-US93-1 Sequence 5, Applicatio	9.12e+01
32	67	4.1	3033	4	US-07-925-0 Sequence 1, Applicatio	9.12e+01
33	67	4.1	3011	8	PCT-US93-0 Sequence 4, Applicatio	9.12e+01
34	67	4.1	69	4	US-08-175-0 Sequence 3, Applicatio	9.12e+01
35	67	4.1	355	6	PCT-US91-0 Sequence 2, Applicatio	9.12e+01
36	67	4.1	782	4	US-07-725-0 Sequence 2, Applicatio	9.12e+01
37	67	4.1	364	8	PCT-US93-1 Sequence 15, Applicati	9.12e+01
38	66	4.0	21	2	US-07-679-0 Sequence 9, Applicatio	1.06e+02
39	66	4.0	477	3	US-07-847-0 Sequence 2, Applicatio	1.06e+02
40	66	4.0	481	4	US-08-186-0 Sequence 2, Applicatio	1.06e+02
41	66	4.0	481	9	PCT-US94-0 Sequence 4, Applicatio	1.06e+02
42	66	4.0	1167	3	US-08-100-0 Sequence 2, Applicatio	1.06e+02
43	66	4.0	18	10	PCT-US95-0 Sequence 187, Applicati	1.06e+02
44	66	4.0	29	9	PCT-US94-0 Sequence 30, Applicati	1.06e+02
45	66	4.0	481	10	PCT-US95-0 Sequence 98, Applicati	1.06e+02

## ALIGNMENTS

RESULT 1  
ID PCT-US93-07545-245 STANDARD; PRT; 28 AA.  
XX -  
AC xxxxxx  
DT 01-JAN-1900  
XX Sequence 245, Application PC/TUS9307545.  
DE Sequence 245, Application PC/TUS9307545.  
XX GENERAL INFORMATION:  
CC APPLICANT: Robert G. Urban  
CC APPLICANT: Roman M. Chicz  
CC APPLICANT: Dario A. A. Vignali  
CC APPLICANT: Mary L. Hedley  
CC APPLICANT: Lawrence J. Stern  
CC APPLICANT: Jack L. Strominger  
CC TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
CC NUMBER OF SEQUENCES: 273  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Fish & Richardson  
CC STREET: 225 Franklin Street  
CC CITY: Boston  
CC STATE: Massachusetts  
CC COUNTRY: U.S.A.  
CC ZIP: 02110-2804  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
CC COMPUTER: IBM PS/2 Model 502 or 55SX  
CC OPERATING SYSTEM: MS-DOS (Version 5.0)  
CC SOFTWARE: WordPerfect (Version 5.1)  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US93/07545  
CC FILING DATE: 19930811  
CC CLASSIFICATION:  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 07/925,460  
CC FILING DATE: August 11, 1992  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Clark, Paul T.  
CC REGISTRATION NUMBER: 30,162  
CC REFERENCE/DOCKET NUMBER: 00246/168001  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (617) 542-5070  
CC TELEFAX: (617) 542-8906  
CC TELEX: 200154  
CC INFORMATION FOR SEQ ID NO: 245:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 28  
CC TYPE: amino acid  
CC STRANDEDNESS:  
CC TOPOLOGY: linear  
CC SEQUENCE 28 AA; 3164 MW; 3693 CN;  
DB 8; Score 219; Match 100.0%; QryMatch 13.3%; Pred. No. 1.40e-11;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 OAKFFACIKRSDGSCAWYGAAPPKQEF 28  
|||||

OY 187 OAKFFACIKRSDGSCAWYGAAPPKQEF 214  
RESULT 2  
ID PCT-US93-07545-246 STANDARD; PRT; 19 AA.  
XX -  
AC xxxxxx  
DT 01-JAN-1900  
XX Sequence 246, Application PC/TUS9307545.  
DE Sequence 246, Application PC/TUS9307545.  
XX GENERAL INFORMATION:  
CC APPLICANT: Robert G. Urban  
CC APPLICANT: Roman M. Chicz  
CC APPLICANT: Dario A. A. Vignali  
CC APPLICANT: Mary L. Hedley  
CC APPLICANT: Lawrence J. Stern  
CC APPLICANT: Jack L. Strominger  
CC TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
CC NUMBER OF SEQUENCES: 273  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Fish & Richardson  
CC STREET: 225 Franklin Street  
CC CITY: Boston  
CC STATE: Massachusetts  
CC COUNTRY: U.S.A.  
CC ZIP: 02110-2804  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
CC COMPUTER: IBM PS/2 Model 502 or 55SX  
CC OPERATING SYSTEM: MS-DOS (Version 5.0)  
CC SOFTWARE: WordPerfect (Version 5.1)  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US93/07545  
CC FILING DATE: 19930811  
CC CLASSIFICATION:  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 07/925,460  
CC FILING DATE: August 11, 1992  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Clark, Paul T.  
CC REGISTRATION NUMBER: 30,162  
CC REFERENCE/DOCKET NUMBER: 00246/168001  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (617) 542-5070  
CC TELEFAX: (617) 542-8906  
CC TELEX: 200154  
CC INFORMATION FOR SEQ ID NO: 246:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 19  
CC TYPE: amino acid  
CC STRANDEDNESS:  
CC TOPOLOGY: linear  
CC SEQUENCE 19 AA; 2238 MW; 1748 CN;  
DB 8; Score 157; Match 100.0%; QryMatch 9.6%; Pred. No. 5.57e-06;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





CC TELEEX: WUI 64470  
 CC INFORMATION FOR SEQ ID NO: 8:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 3033 amino acids  
 CC TYPE: AMINO ACID  
 CC STRANDEDNESS: unknown  
 CC TOPOLOGY: linear  
 CC SEQUENCE 3033 AA; 330178 MW; 48732738 CN;  
 DB 4; Score 91; Match 25.5%; QryMatch 5.5%; Pred. No. 1.68e+00;  
 Matches 24; Conservative 27; Mismatches 37; Indels 6; Gaps 5;  
 Db 2739 IKALACKAAGIVDPVMLVCGDDIIVISESQNEEDERNLRAFTEAMTR--YSAPPGDLP 2796  
 QY 21 LRPAQACSCSP-VHPQAFNCADVIRAKAVSEKVDSGNDIYGNPKRIQYFIKQIKMF 79  
 Db 2797 R-PEYDLELI-TSCSSNV-SVALDSRGRRRYFLT 2827  
 QY 80 KGEKDIETIYAPSSAVCGVSLDVGGKEYLIA 113  
 RESULT 5  
 ID PCT-US95-04656-2 STANDARD; PRT; 990 AA.  
 XX AC xxxxxx  
 XX 01-JAN-1900  
 DE Sequence 2, Application PC/TUS9504656.  
 XX Sequence 2, Application PC/TUS9504656  
 CC GENERAL INFORMATION:  
 CC APPLICANT: Khandke, Kiran M.  
 CC TITLE OF INVENTION: A Novel Protein Designated  
 CC TITLE OF INVENTION: Chondroitinase II and its Use With a Protein Desi  
 CC gnated  
 CC TITLE OF INVENTION: Chondroitinase I to Achieve Complete Vitreal Disi  
 CC nsertion  
 CC NUMBER OF SEQUENCES: 2  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: American Cyanamid Company  
 CC STREET: One Cyanamid Plaza  
 CC CITY: Wayne  
 CC STATE: New Jersey  
 CC COUNTRY: U.S.A.  
 CC ZIP: 07470-8426  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: PCT/US95/04656  
 CC FILING DATE:  
 CC CLASSIFICATION:  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Gordon, Alan M.  
 CC REGISTRATION NUMBER: 30,637  
 CC REFERENCE/DOCKET NUMBER: 32,390-00/PCT  
 CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 201-831-3244  
 CC TELEFAX: 201-831-3305  
 CC INFORMATION FOR SEQ ID NO: 2:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 990 amino acids  
 CC TYPE: amino acid  
 CC TOPOLOGY: linear  
 CC MOLECULE TYPE: protein  
 CC SEQUENCE 990 AA; 111713 MW; 5013050 CN;  
 DB 10; Score 79; Match 32.1%; QryMatch 4.8%; Pred. No. 1.32e+01;  
 Matches 17; Conservative 12; Mismatches 22; Indels 2; Gaps 2;  
 Db 273 GV-FSEGTQKALIDANMLRDVGKTLTQTAIYLRSDLSATDRKKLEERYLLG 323  
 QY 99 GVSVDVGKKEYLIAGKAGDGRMHITLCTDFIVPDTLSTQKSLNHRVQMG 151  
 RESULT 6  
 ID PCT-US94-06430-12 STANDARD; PRT; 476 AA.  
 XX AC xxxxxx  
 XX 01-JAN-1900  
 DE Sequence 12, Application PC/TUS9406430.  
 XX Sequence 12, Application PC/TUS9406430  
 CC GENERAL INFORMATION:  
 CC APPLICANT: The Upjohn Company  
 CC TITLE OF INVENTION: Lettuce Infectious Yellows Virus Genes  
 CC NUMBER OF SEQUENCES: 25  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: The Upjohn Company, Corp. Intellectual  
 CC ADDRESSEE: Property Law  
 CC STREET: 301 Henrietta Street  
 CC CITY: Kalamazoo  
 CC STATE: Michigan  
 CC COUNTRY: USA  
 CC ZIP: 49001  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: PCT/US94/06430  
 CC FILING DATE:  
 CC CLASSIFICATION:  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: Darnley Jr., James D.  
 CC REGISTRATION NUMBER: 33,673  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: 616-385-5210  
 CC TELEFAX: 616-385-6897  
 CC TELEX: 224401  
 CC INFORMATION FOR SEQ ID NO: 12:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 476 amino acids  
 CC TYPE: amino acid

Listing for Mary Hale Tue Feb 6 11:36:52 1996

CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
SQ SEQUENCE 476 AA; 55506 MW; 1217402 CN;  
  
DB 9; Score 79; Match 39.5%; QryMatch 4.8%; Pred. No. 1.32e+01;  
Matches 17; Conservative 7; Mismatches 14; Indels 5; Gaps 3;  
  
Db 256 YEEMVYKMGFSPELYDRFKYTFYFCRAKATCGVDLELGTOR 298  
||: ||| ||| | : ||| : ||| ||| :  
Qy 71 YEIQIKMKR-GPEK-DIEFIYTA---PSSAVCGVSLDVGKK 108  
  
RESULT 7  
ID PCT-US95-06119-14 STANDARD; PRT; 397 AA.  
XX  
AC xxxxxx  
XX  
DT 01-JAN-1900  
XX  
DE Sequence 14, Application PC/TUS9506119.  
XX  
CC Sequence 14, Application PC/TUS9506119  
CC GENERAL INFORMATION:  
CC APPLICANT:  
CC TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE CAPSULAR  
CC TITLE OF INVENTION: POLYSACCHARIDE GENES AND FLANKING REGIONS  
CC NUMBER OF SEQUENCES: 20  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Arnold, White & Durkee  
CC STREET: P.O. Box 4433  
CC CITY: Houston  
CC STATE: TX  
CC COUNTRY: United States of America  
CC ZIP: 77210  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
CC SOFTWARE: PatentIn Release #1.0, Version  
CC SOFTWARE: #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US95/06119  
CC FILING DATE: CONCURRENTLY HERewith  
CC CLASSIFICATION:  
CC PRIOR APPLICATION NUMBER:  
CC APPLICATION NUMBER: US 08/243,546  
CC FILING DATE: 16-MAY-1994  
CC CLASSIFICATION:  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Parker, David L.  
CC REGISTRATION NUMBER: 32,165  
CC REFERENCE/DOCKET NUMBER: AMCY018P---  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (512) 418-3000  
CC TELEFAX: (713) 789-2679  
CC TELEX: 79-0924  
CC INFORMATION FOR SEQ ID NO: 14:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 397 amino acids  
CC TYPE: amino acid

Listing for Mary Hale Tue Feb 6 11:36:52 1996

CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
SQ SEQUENCE 397 AA; 43352 MW; 781935 CN;  
  
DB 10; Score 79; Match 26.1%; QryMatch 4.8%; Pred. No. 1.32e+01;  
Matches 12; Conservative 13; Mismatches 19; Indels 2; Gaps 2;  
  
Db 347 AKSIVSTELVTKIAESYGECLISLQVSNSSLRKFKNLKNITYMF 392  
||: ||| | : ||| : | : ||| | : ||| :  
Qy 47 AKAVSEKE-VDSGNDIYGNP-IKRIQYEIKQIRKMGKGEKDIEFIY 90  
  
RESULT 8  
ID PCT-US94-10357-3 STANDARD; PRT; 928 AA.  
XX  
AC xxxxxx  
XX  
DT 01-JAN-1900  
XX  
DE Sequence 3, Application PC/TUS9410357.  
XX  
CC Sequence 3, Application PC/TUS9410357  
CC GENERAL INFORMATION:  
CC APPLICANT: The Regents of the University of California  
CC APPLICANT: and Canji, Inc.  
CC TITLE OF INVENTION: Therapeutic Use of the Retinoblastoma  
CC TITLE OF INVENTION: Susceptibility Gene Product  
CC NUMBER OF SEQUENCES: 3  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Campbell and Flores  
CC STREET: 4370 La Jolla Village Drive  
CC CITY: San Diego  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 92122  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US94/10357  
CC FILING DATE: 13-SEP-1994  
CC CLASSIFICATION:  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/121,108  
CC FILING DATE: 13-SEP-1993  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Campbell, Cathryn A.  
CC REGISTRATION NUMBER: 31,815  
CC REFERENCE/DOCKET NUMBER: FP-DC 1117  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (619) 535-9001  
CC TELEFAX: (619) 535-8949  
CC INFORMATION FOR SEQ ID NO: 3:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 928 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear

SQ SEQUENCE 928 AA; 106061 MW; 4602767 CN;

DB 9; Score 75; Match 31.3%; QryMatch 4.6%; Pred. No. 2.55e+01;  
Matches 15; Conservative 15; Mismatches 13; Indels 5; Gaps 4;

Db 136 KEIDTSTKV-DNAMSRLIKKYDV-LFALFSKLTCELIYLTOPSSSI 181  
|||:: : |:: |:: : |:: |:: : |:: |:: : |:: |:: :  
QY 53 KEVDGNDIYGNPIKRI--QYEIKQIKMFKGPEKDIEFIY-TAPSSAV 97

RESULT 9  
ID PCT-US94-10357-2 STANDARD; PRT; 928 AA.  
XX AC xxxxxx  
XX DT 01-JAN-1900  
XX DE Sequence 2, Application PC/TUS9410357.  
XX CC Sequence 2, Application PC/TUS9410357  
XX CC GENERAL INFORMATION:  
XX CC APPLICANT: The Regents of the University of California  
XX CC APPLICANT: and Canji, Inc.  
XX CC TITLE OF INVENTION: Therapeutic Use of the Retinoblastoma  
XX CC TITLE OF INVENTION: Susceptibility Gene Product  
XX CC NUMBER OF SEQUENCES: 3  
XX CC CORRESPONDENCE ADDRESS:  
XX CC ADDRESSEE: Campbell and Flores  
XX CC STREET: 4370 La Jolla Village Drive  
XX CC CITY: San Diego  
XX CC STATE: California  
XX CC COUNTRY: USA  
XX CC ZIP: 92122  
XX CC COMPUTER READABLE FORM:  
XX CC MEDIUM TYPE: Floppy disk  
XX CC COMPUTER: IBM PC compatible  
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS  
XX CC SOFTWARE: Patent In Release #1.0, Version #1.25  
XX CC CURRENT APPLICATION DATA:  
XX CC APPLICATION NUMBER: PCT/US94/10357  
XX CC FILING DATE: 13-SEP-1994  
XX CC CLASSIFICATION:  
XX CC PRIOR APPLICATION DATA:  
XX CC APPLICATION NUMBER: US 08/121,108  
XX CC FILING DATE: 13-SEP-1993  
XX CC ATTORNEY/AGENT INFORMATION:  
XX CC NAME: Campbell, Cathryn A.  
XX CC REGISTRATION NUMBER: 31,815  
XX CC REFERENCE/DOCKET NUMBER: FP-UC 1117  
XX CC TELECOMMUNICATION INFORMATION:  
XX CC TELEPHONE: (619) 535-9001  
XX CC TELEFAX: (619) 535-8949  
XX CC INFORMATION FOR SEQ ID NO: 2:  
XX CC SEQUENCE CHARACTERISTICS:  
XX CC LENGTH: 928 amino acids  
XX CC TYPE: amino acid  
XX CC TOPOLOGY: linear  
XX CC MOLECULE TYPE: protein  
SQ SEQUENCE 928 AA; 106144 MW; 4604196 CN;

DB 9; Score 75; Match 31.3%; QryMatch 4.6%; Pred. No. 2.55e+01;  
Matches 15; Conservative 15; Mismatches 13; Indels 5; Gaps 4;

Db 136 KEIDTSTKV-DNAMSRLIKKYDV-LFALFSKLTCELIYLTOPSSSI 181  
|||:: : |:: |:: : |:: |:: : |:: |:: : |:: |:: :  
QY 53 KEVDGNDIYGNPIKRI--QYEIKQIKMFKGPEKDIEFIY-TAPSSAV 97

RESULT 10  
ID PCT-US95-05744-13 STANDARD; PRT; 490 AA.  
XX AC xxxxxx  
XX DT 01-JAN-1900  
XX DE Sequence 13, Application PC/TUS9505744.  
XX CC Sequence 13, Application PC/TUS9505744  
XX CC GENERAL INFORMATION:  
XX CC APPLICANT: GOLDSTEIN, Joyce A.  
XX CC APPLICANT: ROMKES-SPARKS, Marjorie  
XX CC APPLICANT: DE MORAIS, Sonia M.F.  
XX CC TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN  
XX CC TITLE OF INVENTION: CYTOCHROME P450 2C19: THE PRINCIPAL DETERMINANT  
XX CC TITLE OF INVENTION: OF S-MEPHNYNTOIN METABOLISM  
XX CC NUMBER OF SEQUENCES: 61  
XX CC CORRESPONDENCE ADDRESS:  
XX CC ADDRESSEE: Townsend and Townsend Khourie and Crew  
XX CC STREET: 379 Lytton Avenue  
XX CC CITY: Palo Alto  
XX CC STATE: California  
XX CC COUNTRY: US  
XX CC ZIP: 94301  
XX CC COMPUTER READABLE FORM:  
XX CC MEDIUM TYPE: Floppy disk  
XX CC COMPUTER: IBM PC compatible  
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS  
XX CC SOFTWARE: Patent In Release #1.0, Version #1.25  
XX CC CURRENT APPLICATION DATA:  
XX CC APPLICATION NUMBER: PCT/US95/05744  
XX CC FILING DATE:  
XX CC CLASSIFICATION:  
XX CC PRIOR APPLICATION DATA:  
XX CC APPLICATION NUMBER: US 08/238,821  
XX CC FILING DATE: 06-MAY-1994  
XX CC PRIOR APPLICATION DATA:  
XX CC APPLICATION NUMBER: US 08/201,118  
XX CC FILING DATE: 22-FEB-1994  
XX CC PRIOR APPLICATION DATA:  
XX CC APPLICATION NUMBER: US 07/864,962  
XX CC FILING DATE: 09-APR-1992  
XX CC ATTORNEY/AGENT INFORMATION:  
XX CC NAME: Dow, Karen B.  
XX CC REGISTRATION NUMBER: 29,684  
XX CC REFERENCE/DOCKET NUMBER: 15280-192-1-1  
XX CC TELECOMMUNICATION INFORMATION:  
XX CC TELEPHONE: (415) 326-2400  
XX CC TELEFAX: (415) 326-2422  
XX CC INFORMATION FOR SEQ ID NO: 13:  
XX CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 490 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC HYPOTHETICAL: YES

SQ SEQUENCE 490 AA; 55708 MW; 1357717 CN;

DB 10; Score 74; Match 25.6%; QryMatch 4.5%; Pred. No. 3.00e+01;  
Matches 21; Conservative 20; Mismatches 37; Indels 4; Gaps 4;

Db 1 MDPXV-VLVLCISCLLLSLWROSGRGKLPGLPPIXPXIGNILQIDKDIS-KSLFNXS 58

Qy 1 MGAARTLRALGLLLLATLLRPADACSPVHPQQAFCNADVV-IRAKAVSEKVDSGN 59

Db 59 KVIYGVFTFYFGIKRPIVVLHG 79

Qy 60 DIYGNPIKRIQYIKQIKMFKG 81

RESULT 11

ID PCT-US93-03076-4 STANDARD; PRT; 778 AA.

XX AC xxxxxx

XX AC xxxxxx

XX DT 01-JAN-1900

XX DT 01-JAN-1900

XX DE Sequence 4, Application PC/TUS9303076.

XX DE Sequence 4, Application PC/TUS9303076.

XX CC GENERAL INFORMATION:

XX CC APPLICANT: Whitehead Institute for Biomedical Research

XX CC TITLE OF INVENTION: GAP-Associated Protein p190 and

XX CC TITLE OF INVENTION: Transduction

XX CC NUMBER OF SEQUENCES: 20

XX CC CORRESPONDENCE ADDRESS:

XX CC ADDRESSEE: Hamilton, Brook, Smith &amp; Reynolds, P.C.

XX CC STREET: 2 Militia Drive

XX CC CITY: Lexington

XX CC STATE: MA

XX CC COUNTRY: US

XX CC ZIP: 02173

XX CC COMPUTER READABLE FORM:

XX CC MEDIUM TYPE: Floppy disk

XX CC COMPUTER: IBM PC compatible

XX CC OPERATING SYSTEM: PC-DOS/MS-DOS

XX CC SOFTWARE: Patent in Release #1.0, Version #1.25

XX CC CURRENT APPLICATION DATA:

XX CC APPLICATION NUMBER: PCT/US93/03076

XX CC FILING DATE: 19930331

XX CC CLASSIFICATION:

XX CC ATTORNEY/AGENT INFORMATION:

XX CC NAME: Granahan, Patricia

XX CC REGISTRATION NUMBER: 32,227

XX CC REFERENCE/DOCKET NUMBER: WHI92-03A

XX CC TELECOMMUNICATION INFORMATION:

XX CC TELEPHONE: 617-861-6240

XX CC TELEFAX: 617-861-9540

XX CC INFORMATION FOR SEQ ID NO: 4:

XX CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 778 amino acids

CC TYPE: AMINO ACID

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

SQ SEQUENCE 778 AA; 87981 MW; 3142889 CN;

DB 8; Score 74; Match 24.3%; QryMatch 4.5%; Pred. No. 3.00e+01;  
Matches 17; Conservative 12; Mismatches 37; Indels 4; Gaps 4;

Db 159 KHIHFVH-PKTCPCPCACVDAKIEHLISSRFIRPSDRNQKNSLSDNIDRLNVLIG 217

Qy 84 KDIEFIYAPSSAVCGVSLD-VGKKEYLIAGK-AEGDGKWHI-TLCDFIVPMDTLSTTQ 140

Db 218 KDALPESWPM 227

Qy 141 KKSLSNRYQM 150

RESULT 12

ID US-07-803-636A-2 STANDARD; PRT; 480 AA.

XX AC xxxxxx

XX AC xxxxxx

XX DT 01-JAN-1900

XX DT 01-JAN-1900

XX DE Sequence 2, Application US/07803636A.

XX DE Sequence 2, Application US/07803636A.

XX CC GENERAL INFORMATION:

XX CC APPLICANT: MCGUIRE, TRAVIS C., TERRY F. McELWAIN, LANCE E. PERRYMAN,

XX CC APPLICANT: WILLIAM C. DAVIS

XX CC TITLE OF INVENTION: IMMUNIZATION AGAINST BABESIOSIS USING

XX CC TITLE OF INVENTION: PURIFIED SURFACE ANTIGENS OF BABESIA BIGEMINA AND

XX CC SIMILAR

XX CC NUMBER OF SEQUENCES: 2

XX CC CORRESPONDENCE ADDRESS:

XX CC ADDRESSEE: DAVID R. SALIWANCHIK

XX CC STREET: 2421 NW 41ST STREET, SUITE A-1

XX CC CITY: GAINESVILLE

XX CC STATE: FLORIDA

XX CC COUNTRY: USA

XX CC ZIP: 32606

XX CC COMPUTER READABLE FORM:

XX CC MEDIUM TYPE: Floppy disk

XX CC COMPUTER: IBM PC compatible

XX CC OPERATING SYSTEM: PC-DOS/MS-DOS

XX CC SOFTWARE: Patent in Release #1.0, Version #1.25

XX CC CURRENT APPLICATION DATA:

XX CC APPLICATION NUMBER: US/07/803,636A

XX CC FILING DATE: 19911206

XX CC CLASSIFICATION: 424

XX CC ATTORNEY/AGENT INFORMATION:

XX CC NAME: SALIWANCHIK, DAVID R

XX CC REGISTRATION NUMBER: 31,794

XX CC REFERENCE/DOCKET NUMBER: WA4-059.C1

XX CC TELECOMMUNICATION INFORMATION:

XX CC TELEPHONE: 904-375-8100

XX CC TELEFAX: 904-372-5800

XX CC INFORMATION FOR SEQ ID NO: 2:



QY 47 AKAVSEKVDGNDIYGNPIKRIQYEIKQIKMKFGPKDI 86  
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RESULT 14  
ID PCT-US95-05008-8 STANDARD; PRT; 659 AA.  
XX  
AC xxxxxx  
XX  
DT 01-JAN-1900  
XX  
DE Sequence 8, Application PC/TUS9505008.  
XX  
CC Sequence 8, Application PC/TUS9505008  
CC GENERAL INFORMATION:  
CC APPLICANT: Sugen, Inc.  
CC APPLICANT: 515 Galveston Drive  
CC APPLICANT: Redwood City, California 94063-4720  
CC APPLICANT: United States of America  
CC APPLICANT: Wissenschaften E.V.  
CC APPLICANT: Hofgarten Str. 2  
CC APPLICANT: Munchen 80539  
CC APPLICANT: Germany  
CC TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine  
CC TITLE OF INVENTION: Kinases  
CC NUMBER OF SEQUENCES: 21  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Pennie & Edmonds  
CC STREET: 1155 Avenue of the Americas  
CC CITY: New York  
CC STATE: New York  
CC COUNTRY: U.S.A.  
CC ZIP: 10036  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US95/05008  
CC FILING DATE: 24-APR-1995  
CC CLASSIFICATION:  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/232,545  
CC FILING DATE: 22-APR-1994  
CC CLASSIFICATION:  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Coruzzi, Laura A.  
CC REGISTRATION NUMBER: 30,742  
CC REFERENCE/DOCKET NUMBER: 7683-074  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (212) 790-9090  
CC TELEFAX: (212) 869-9741  
CC TELEX: 66141 PENNIE  
CC INFORMATION FOR SEQ ID NO: 8:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 659 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: unknown  
CC TOPOLOGY: unknown

CC MOLECULE TYPE: protein  
SQ SEQUENCE 659 AA; 76281 MW; 2353510 CN;  
DB 10; Score 71; Match 47.8%; QryMatch 4.3%; Pred. No. 4.86e+01;  
Matches 11; Conservative 5; Mismatches 5; Indels 2; Gaps 2;  
Db 422 RGQYDV-AIKMIKEGSMSEDEFI 443  
| |||: |||| |:: || | ::|| ::||  
QY 68 RIQYEIKQIKMKF-GPEKDIEFI 89  
XX  
DE Sequence 1, Application PC/TUS9301652.  
XX  
CC Sequence 1, Application PC/TUS9301652  
CC GENERAL INFORMATION:  
CC APPLICANT: Bouck, Noel P.  
CC APPLICANT: Polverini, Peter J.  
CC APPLICANT: Good, Deborah J.  
CC APPLICANT: Frazier, William A.  
CC TITLE OF INVENTION: Method and Composition for  
CC TITLE OF INVENTION: Inhibiting Angiogenesis  
CC NUMBER OF SEQUENCES: 12  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut  
CC STREET: 100 South Wacker Drive, Suite 960  
CC CITY: Chicago  
CC STATE: Illinois  
CC COUNTRY: USA  
CC ZIP: 60606-4002  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US93/01652  
CC FILING DATE: 19930222  
CC CLASSIFICATION:  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US/07/841,656  
CC FILING DATE: 24-FEB-1992  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US/07/464,369  
CC FILING DATE: 12-JAN-1990  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Fentress, Susan B.  
CC REGISTRATION NUMBER: 31,327  
CC REFERENCE/DOCKET NUMBER: 92005-PCT  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (312)-456-8000  
CC TELEFAX: (312)-456-7776  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:



CC LENGTH: 239 amino acids  
 CC TYPE: AMINO ACID  
 CC STRANDEDNESS: unknown  
 CC TOPOLOGY: unknown  
 CC MOLECULE TYPE: peptide  
 SQ SEQUENCE 239 AA; 26213 MW; 275594 CN;

DB 8; Score 70; Match 47.6%; QryMatch 4.3%; Pred. No. 5.70e+01;  
 Matches 10; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

Ds 37 CKKVCPIPCSNATVPDGE 57

Qy 154 CKITRCPIPCYISS-PD-EC 172

Search completed: Mon Feb 5 17:01:42 1996  
 Job time : 10 secs.

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W P S R L H (TM)

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Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MParch\_pp protein - protein database search, using Smith-Waterman algorithm  
 Run on: Mon Feb 5 17:02:03 1996; MasPar time 13.15 Seconds  
 Tabular output not generated. 195.746 Million cell updates/sec

Title: >FIG2  
 Description: (1:220) from trans.pep  
 Perfect Score: 1643  
 Sequence: 1 MGAARTLRALGLLLATL.....CAWYRGAAPPKQEFIDIEDP 220

Scoring table: PAM 150  
 Gap 11

Searched: 131564 seqs, 11696421 residues

Database: a-pending  
 1 PCT91  
 2 PCT92  
 3 PCT93  
 4 PCT94  
 5 PCT95  
 6 PCT96  
 7 U73  
 8 U74  
 9 U75  
 10 U76

11 U771  
 12 U772  
 13 U781  
 14 U782  
 15 U791  
 16 U792  
 17 U800  
 18 U801  
 19 U802  
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 60 U843  
 61 U844  
 62 U845  
 63 U846  
 64 U847  
 65 U848  
 66 U849  
 67 U85  
 68 U60  
 69 NEWP  
 70 NEW08

Statistics: Mean 30.214; Variance 114.839; scale 0.263

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1643	100.0	220	33	US-08-167-Sequence 10, Applicati	1.12e-168
2	1607	97.8	220	33	US-08-167-Sequence 11, Applicati	1.24e-164
3	1550	94.3	220	33	US-08-167-Sequence 12, Applicati	3.16e-158
4	844	51.4	224	4	PCT-US94-1 Sequence 2, Applicati	2.19e-79
5	695	42.3	211	4	PCT-US94-1 Sequence 13, Applicati	6.06e-63
6	695	42.3	211	4	PCT-US94-1 Sequence 13, Applicati	6.06e-63
7	695	42.3	211	4	PCT-US94-1 Sequence 2, Applicati	6.06e-63
8	695	42.3	211	4	PCT-US94-1 Sequence 2, Applicati	6.06e-63
9	686	41.8	212	33	US-08-167-Sequence 13, Applicati	5.91e-62
10	686	41.8	211	33	US-08-167-Sequence 14, Applicati	5.91e-62
11	685	41.7	198	4	PCT-US94-1 Sequence 15, Applicati	7.61e-62
12	685	41.7	198	4	PCT-US94-1 Sequence 15, Applicati	7.61e-62
13	673	41.0	188	33	US-08-167-Sequence 1, Applicati	1.58e-60
14	556	33.8	164	30	US-08-134-Sequence 17, Applicati	9.90e-48
15	556	33.8	164	30	US-08-134-Sequence 17, Applicati	9.90e-48
16	521	31.7	207	33	US-08-167-Sequence 6, Applicati	6.31e-44
17	518	31.5	206	33	US-08-167-Sequence 7, Applicati	1.33e-43
18	517	31.5	205	33	US-08-167-Sequence 4, Applicati	1.71e-43
19	506	30.8	207	33	US-08-167-Sequence 8, Applicati	2.67e-42
20	488	29.7	207	33	US-08-167-Sequence 9, Applicati	2.37e-40
21	476	29.0	207	33	US-08-167-Sequence 5, Applicati	4.69e-39
22	470	28.6	125	33	US-08-167-Sequence 16, Applicati	2.08e-38
23	219	13.3	28	65	US-08-488-Sequence 245, Applicat	5.29e-12
24	219	13.3	28	65	US-08-488-Sequence 245, Applicat	5.29e-12
25	219	13.3	28	24	US-08-077-Sequence 245, Applicat	5.29e-12
26	219	13.3	28	24	US-08-077-Sequence 245, Applicat	5.29e-12
27	219	13.3	28	65	US-08-488-Sequence 245, Applicat	5.29e-12
28	219	13.3	28	64	US-08-476-Sequence 245, Applicat	5.29e-12
29	219	13.3	28	65	US-08-480-Sequence 245, Applicat	5.29e-12
30	219	13.3	28	64	US-08-475-Sequence 245, Applicat	5.29e-12
31	157	9.6	19	63	US-08-488-Sequence 246, Applicat	6.71e-06
32	157	9.6	19	63	US-08-488-Sequence 246, Applicat	6.71e-06
33	157	9.6	19	64	US-08-475-Sequence 246, Applicat	6.71e-06
34	157	9.6	19	64	US-08-476-Sequence 246, Applicat	6.71e-06
35	157	9.6	19	65	US-08-480-Sequence 246, Applicat	6.71e-06
36	157	9.6	19	65	US-08-487-Sequence 246, Applicat	6.71e-06
37	157	9.6	19	24	US-08-077-Sequence 246, Applicat	6.71e-06
38	157	9.6	19	24	US-08-077-Sequence 246, Applicat	6.71e-06
39	138	8.4	25	64	US-08-474-Sequence 21, Applicati	1.85e-03
40	131	8.0	18	33	US-08-167-Sequence 19, Applicati	3.45e-02
41	117	7.1	18	33	US-08-167-Sequence 19, Applicati	3.45e-02
42	116	7.1	18	33	US-08-167-Sequence 19, Applicati	4.24e-02
43	100	6.1	28	31	US-08-141-Sequence 1, Applicati	1.06e+00
44	99	6.0	18	33	US-08-167-Sequence 20, Applicati	1.29e+00
45	96	5.8	76	67	US-08-538-Sequence 4, Applicati	2.32e+00

ALIGNMENTS

RESULT 1  
ID US-08-167-463-10 STANDARD; PRT; 220 AA.

XX AC xxxxxx

XX DT 01-JAN-1900

XX DE Sequence 10, Application US/08167463.

XX CC Sequence 10, Application US/08167463

CC GENERAL INFORMATION:

CC APPLICANT: HAWKES, SUSAN P.

CC APPLICANT: KISHANI, NARENDRA S.

CC APPLICANT: YANG, TE-TUAN

CC TITLE OF INVENTION: HUMAN TIMP-3

CC NUMBER OF SEQUENCES: 32

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: MORRISON & FOERSTER

CC STREET: 755 Page Mill Road

CC CITY: Palo Alto

CC STATE: California

CC COUNTRY: USA

CC ZIP: 94304-1018

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent In Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/167,463

CC FILING DATE: 13-DEC-1993

CC CLASSIFICATION: 530

CC ATTORNEY/AGENT INFORMATION:

CC NAME: LEHNHARDT, SUSAN K.

CC REGISTRATION NUMBER: 33,943

CC REFERENCE/DOCKET NUMBER: 22000-20542.20

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (415) 813-5600

CC TELEFAX: (415) 494-0792

CC TELEX: 706141

CC INFORMATION FOR SEQ ID NO: 10:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 220 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC SEQUENCE 220 AA; 24399 MW; 242975 CN;

DB 33; Score 1643; Match 100.0%; QryMatch 100.0%; Pred. No. 1.12e-168; Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MCAARTLRALGILLATILRPADACSPVHPQQAFCNADVIRAKVSEKVDSDND 60

QY 1 MCAARTLRALGILLATILRPADACSPVHPQQAFCNADVIRAKVSEKVDSDND 60

Db 61 IYGNPKRIQEIQIKMFKGPEKIDIEFIYTPASSVCGVSLDVGGKKEYLIAGKAE 120

QY 61 IYGNPKRIQEIQIKMFKGPEKIDIEFIYTPASSVCGVSLDVGGKKEYLIAGKAE 120

BONET PROXY

Listing for Mary Hale Tue Feb 6 11:36:53 1996

Db 121 KMHTLCLDFIVPMDTSTTQKSLNHRVOMGCECKITRCPMPCYISSPDECLMDWVTE 180  
Qy 121 KMHTLCLDFIVPMDTSTTQKSLNHRVOMGCECKITRCPMPCYISSPDECLMDWVTE 180  
Db 181 KNINGHOAKFFACIKRSDGSCAWYRGAPPKQEFFLDIEDP 220  
Qy 181 KNINGHOAKFFACIKRSDGSCAWYRGAPPKQEFFLDIEDP 220

RESULT 2  
ID US-08-167-463-11 STANDARD; PRT; 220 AA.

XX AC xxxxxx  
XX DT 01-JAN-1900  
XX DE Sequence 11, Application US/08167463.

XX CC Sequence 11, Application US/08167463  
CC GENERAL INFORMATION:  
CC APPLICANT: HAWKES, SUSAN P.  
CC APPLICANT: KISHNANI, NARENDRA S.  
CC APPLICANT: YANG, TE-TUAN  
CC TITLE OF INVENTION: HUMAN TIMP-3  
CC NUMBER OF SEQUENCES: 32  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: MORRISON & FOERSTER  
CC STREET: 755 Page Mill Road  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94304-1018  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/167,463  
CC FILING DATE: 13-DEC-1993  
CC CLASSIFICATION: 530  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: LEHNHARDT, SUSAN K.  
CC REGISTRATION NUMBER: 33,943  
CC REFERENCE/DOCKET NUMBER: 22000-20542.20  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 813-5600  
CC TELEFAX: (415) 494-0792  
CC TELEX: 706141  
CC INFORMATION FOR SEQ ID NO: 11:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 220 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
SQ SEQUENCE 220 AA; 24367 MW; 243101 CN;

DB 33; Score 1607; Match 96.8%; QryMatch 97.8%; Pred. No. 1.24e-164;  
Matches 213; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Listing for Mary Hale Tue Feb 6 11:36:53 1996

Db 1 MGAARSURIAHGLLLASLLRPADACSCSPVHPQOAFCNADVIRAKAVSEKEVDSGND 60  
Qy 1 MGAARSURIAHGLLLASLLRPADACSCSPVHPQOAFCNADVIRAKAVSEKEVDSGND 60  
Db 61 IYGNP IKRIQYIEIKRIMFKGPKDIEFIYAPSSAVCGVSLDVGKKEYLIAGKAEGDG 120  
Qy 61 IYGNP IKRIQYIEIKRIMFKGPKDIEFIYAPSSAVCGVSLDVGKKEYLIAGKAEGDG 120  
Db 121 KMHTLCLDFIVPMDTSTTQKSLNHRVOMGCECKITRCPMPCYISSPDECLMDWVTE 180  
Qy 121 KMHTLCLDFIVPMDTSTTQKSLNHRVOMGCECKITRCPMPCYISSPDECLMDWVTE 180  
Db 181 KNINGHOAKFFACIKRSDGSCAWYRGAPPKQEFFLDIEDP 220  
Qy 181 KNINGHOAKFFACIKRSDGSCAWYRGAPPKQEFFLDIEDP 220

RESULT 3  
ID US-08-167-463-12 STANDARD; PRT; 220 AA.

XX AC xxxxxx  
XX DT 01-JAN-1900  
XX DE Sequence 12, Application US/08167463.

XX CC Sequence 12, Application US/08167463  
CC GENERAL INFORMATION:  
CC APPLICANT: HAWKES, SUSAN P.  
CC APPLICANT: KISHNANI, NARENDRA S.  
CC APPLICANT: YANG, TE-TUAN  
CC TITLE OF INVENTION: HUMAN TIMP-3  
CC NUMBER OF SEQUENCES: 32  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: MORRISON & FOERSTER  
CC STREET: 755 Page Mill Road  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94304-1018  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/167,463  
CC FILING DATE: 13-DEC-1993  
CC CLASSIFICATION: 530  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: LEHNHARDT, SUSAN K.  
CC REGISTRATION NUMBER: 33,943  
CC REFERENCE/DOCKET NUMBER: 22000-20542.20  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (415) 813-5600  
CC TELEFAX: (415) 494-0792  
CC TELEX: 706141  
CC INFORMATION FOR SEQ ID NO: 12:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 220 amino acids

CC		TYPE: amino acid	
CC		STRANDEDNESS: single	
CC		TOPOLOGY: linear	
SQ	SEQUENCE	220 AA; 24355 MW; 234318 CN;	
DB	33; Score	1550; Match 91.8%; OryMatch 94.3%; Pred. No. 3.16e-158;	
Matches	202; Conservative	12; Mismatches 6; Indels 0; Gaps 0;	
Db	1	MGAARSPLAFCLLLGLTLLPRADSCSPVHPQQAFCNADIVIRAKAVNKKEVDSGND 60	
Qy	1	MGAARTLRLALGELLALLTLRPADACSCSPVHPQQAFCNADVIRAKAVSEKVEDSGND 60	
Db	61	IYGNPIKRIOEIKOIKMFKGPDODIEFIYTAPAAVCGVSIDIGKKKEYILLIAGKAEGNG 120	
Qy	61	IYGNPIKRIOEIKOIKMFKGPEKDIEFIYTAPSSAVCGVSIDVGKKKEYILLIAGKAEGDG 120	
Db	121	NMHITLCDFIVPMDTLSATOKKSINHRYOMGCECKITRCMPICPVISSPDFECLMWDWYTE 180	
Qy	121	NMHITLCDFIVPMDTLSTTKKSINHRYOMGCECKITRCMPICPVISSPDFECLMWDWYTE 180	
Db	181	KNINGHOAKTFACIKRSDGSCAWYRGAAAPPKQEFDIEDP 220	
Qy	181	KNINGHOAKTFACIKRSDGSCAWYRGAAAPPKQEFDIEDP 220	
RESULT	4		
ID	PCT-US94-14498A-2	STANDARD; PRT; 224 AA.	
XX	xxxxxx		
XD	01-JAN-1900		
DT			
XX			
DE			
XX			
CC	Sequence 2, Application PC/TUS9414498A.		
CC	GENERAL INFORMATION:		
CC	APPLICANT: GREENE, ET AL.		
CC	TITLE OF INVENTION: Human TIMP-4		
CC	NUMBER OF SEQUENCES: 2		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN,		
CC	ADDRESSEE: CECCHI, STEWART & OLSTEIN		
CC	STREET: 6 BECKER FARM ROAD		
CC	CITY: ROSELAND		
CC	STATE: NEW JERSEY		
CC	COUNTRY: USA		
CC	ZIP: 07068		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: 3.5 INCH DISKETTE		
CC	COMPUTER: IBM PS/2		
CC	OPERATING SYSTEM: MS-DOS		
CC	SOFTWARE: WORD PERFECT 5.1		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: PCT/US94/14498A		
CC	FILING DATE: Submitted herewith		
CC	CLASSIFICATION:		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER:		
CC	FILING DATE:		
CC	ATTORNEY/AGENT INFORMATION:		

CC	NAME: FERRARO, GREGORY D.	
CC	REGISTRATION NUMBER: 36,134	
CC	REFERENCE/DOCKET NUMBER: 325800-278	
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE: 201-994-1700	
CC	TELEFAX: 201-994-1744	
CC	INFORMATION FOR SEQ ID NO: 2:	
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH: 224 AMINO ACIDS	
CC	TYPE: AMINO ACID	
CC	STRANDEDNESS:	
CC	TOPOLOGY: LINEAR	
CC	MOLECULE TYPE: PROTEIN	
CC	SEQUENCE 224 AA; 25502 MW; 274373 CN;	
DB	4; Score 844; Match 48.2%; QryMatch 51.4%; Pred. No. 2,19e-79;	
Matches	109; Conservative 53; Mismatches 56; Indels 8; Gaps 5;	
Db	1 MFGSRPAP-SWILLRLALLRPPGLGEACSCAPAHPOQHICHSAIVIRAKISSEKVP 59	
Qy	1 MGAARTLRALGULL-LATLRPA--DACSCSPVHPQAFNCADVIVIRAKAVSEKVD 56	
Db	60 ASADP-ADTERMLRYEIKQIMKFGFKVDQVIYTPDSSLGCGKLEANSQRYLLTG 118	
Qy	57 SGNDIYGNPIKRIQYEIKQIMKFGPEK--DIEFYIATPSSAVCGSLDVGKKEYLIAG 114	
Db	119 QVLSGKVFTHLCHNYIEPWEDLSILVQRESLNHHYHLNCCQITTCYTPCTISAPNCLW 178	
Qy	115 KAEGDKRMHITLCSDFIVPMDTSLTQKKSINHRYQMGCECKTITRCPMIPCYISSPDECLW 174	
Db	179 TDWLLERKLYGVQAHVCKMKHVDGTCSWYRGHLPLRKEFVDIVOP 224	
Qy	175 MDWVTEKRNHGQAKFFACIKRSDGSCAWYRGAAPKQFLDIEDP 220	
RESULT	5	
ID	PCT-US94-11241-13	STANDARD; PRT; 211 AA.
AC	xxxxxx	
DT	01-JAN-1900	
XX	Sequence 13, Application PC/TUS9411241.	
DE	Sequence 13, Application PC/TUS9411241	
CC	GENERAL INFORMATION:	
CC	APPLICANT: Silbiger, Scott M.	
CC	APPLICANT: Koski, Raymond A.	
CC	TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type	
CC	TITLE OF INVENTION: Three (TIMP-3) Composition and Methods	
CC	NUMBER OF SEQUENCES: 21	
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESS: Amgen Inc./Patent Operations/RMP	
CC	STREET: 1840 Dehavilland Drive	
CC	CITY: Thousand Oaks	
CC	STATE: California	
CC	COUNTRY: USA	
CC	ZIP: 91320-1789	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE: Floppy disk	

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CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/11241
CC FILING DATE:
CC CLASSIFICATION:
CC INFORMATION FOR SEQ ID NO: 13:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 211 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 211 AA; 24145 MW; 244095 CN;

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[illegible][illegible]

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0.  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/134,231  
FILING DATE:  
CLASSIFICATION: 424  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 211 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE 211 AA: 24145 MW: 244095 CN:

DB 30s	Score	695;	Match	43.6%;	QryMatch	42.3%;	Pred. No.	6.06e-63;	
Matches	95;	Conservative	56;	Mismatches	55;	Indels	12;	Gaps	10;
Db	2	TPWLGILVILGWSIGDWAECTSPSPHQDAFNCSDIVIRAKVVGKKLVKEGF--	FGT	59					
Qy	7	TLRLALGILLLA-TLL-RPADACSCSPVHPQQAFQCNADVIRAKAVSEKVEDSGNDIYGN	64						
Db	60	-L--V-YTIKKMRYGFTKMPHVOYIHTAESISGLGKLEVN-KYQVILLTGRYV-DGKM	113						
Qy	65	PIKRIQYIKQIMFKG--PEK-DIEFYITAPSAVGVSLDVGKGKLYIAGKAEGDGKM	122						
Db	114	YTGICNFVERWDQLTLSQRKGLNRYHLGNCNKKIKCYLPCFVTSKNECLWTDLMSNFG	173						
Qy	123	HITLCDFIVPMDTLSTQKSLNHRHYQMGECKLITCPMIPCYISSPDECLMDWDWVTEKN	182						
Db	174	YFGYSKHVACIRQGGYCSWYRGWAPPPDKSIINATDP	211						
Qy	183	INGHOAKYFACIKRSDGSCAWYRGAPPKQEFFLDIEDP	220						

RESULT		7	PCT-US94-11599-2	STANDARD;	PRT;	211 AA.
ID	XX		AC			
	XX		xxxxxx			
DT	XX		01-JAN-1900			
DE	XX					
	XX		Sequence 2, Application PC/TUS9411599.			
	CC		Sequence 2, Application PC/TUS9411599			
	CC		GENERAL INFORMATION:			
	CC		APPLICANT: Incyte Pharmaceuticals, Inc.			
	CC		APPLICANT: 3330 Hillview Avenue			
	CC		APPLICANT: Palo Alto, California 94304			
	CC		APPLICANT: United States of America			
	CC		TITLE OF INVENTION: Novel Human Monocyte/Macrophage-Derived Proteinase Inhibitor			
	CC		TITLE OF INVENTION: Metalloproteinase Inhibitors			
	ses					
	CC		NUMBER OF SEQUENCES: 6			
	CC		CORRESPONDENCE ADDRESS:			
	CC		ADDRESSEE: Pennie and Edmonds			
	CC		STREET: 1155 Avenue of the Americas			
	CC		CITY: New York			

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CC STATE: California
CC COUNTRY: United States of America
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/11599
CC FILING DATE: 07-OCT-1994
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Halluin, Albert P.
CC REGISTRATION NUMBER: 25,227
CC REFERENCE/DOCKET NUMBER: 8135-041
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-854-3660
CC TELEFAX: 415-854-3694
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 211 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC IMMEDIATE SOURCE:
CC CLONE: T-012006
CC SEQUENCE 211 AA; 24145 MW; 244095 CN;

DB 4; Score 695; Match 43.6%; QryMatch 42.3%; Pred. No. 6.06e-63;
Matches 95; Conservative 56; Mismatches 55; Indels 12; Gaps 10;

Db 2 TPWGLIVLIGSLDNGAEACTCSPHPQDAFCNSDIVIRAKVGVKLVKEGP--FGT 59
Qy 7 TRLALGLLLA-TLL-RPADACSCSPVHPQAFCNADVIRAKAVSEKVEDSGNDIYN 64

Db 60 -L--V-YTIKQMYRGFTKMPHVQYIHTASESLCGKLEVN-KYQYILTGRVY-DGKM 113
Qy 65 PIKRIQYEIKQIKMFKG-PEK-DIEFIYTPSSAVCGVSLDVGKKEVLIAGKAEKGDM 122
Db 114 YTGICNFVERWDLTSLQKGLNRYHLGCNCKIKSCYILPCFVTSKNECLWTDMLSNFG 173
Qy 123 HITLCDFIVPWDTLTSTQKSLNRYQMGCECKITRCMPICYISSPDECLMDWDWTEKN 182

Db 174 YPGYQSKHACIRQKGYCSWYRGWAPDPKSIINATDP 211
Qy 183 INGHQAKFTACIKRSDGSAWYRGAAAPKPKFIEDIEDP 220

RESULT 8
ID US-08-319-555-2 STANDARD; PRT; 211 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 2, Application US/08319555.
XX
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CC Sequence 2, Application US/08319555
CC GENERAL INFORMATION:
CC APPLICANT: Scott, Randal W.
CC APPLICANT: Levine, Wendy B.
CC APPLICANT: Seilhamer, Jeffrey J.
CC APPLICANT: Delegeane, Angelo M.
CC TITLE OF INVENTION: Novel Human Monocyte/Macrophage Derived
CC TITLE OF INVENTION: Metalloproteinase Inhibitor, Its Production And U
ses
CC NUMBER OF SEQUENCES: 4
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/319,555
CC FILING DATE: 07-OCT-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/133,956
CC FILING DATE: 07-OCT-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Halluin, Albert P.
CC REGISTRATION NUMBER: 25,227
CC REFERENCE/DOCKET NUMBER: 8135-041-999
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-854-3660
CC TELEFAX: 415-854-3694
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 211 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 211 AA; 24145 MW; 244095 CN;

DB 48; Score 695; Match 43.6%; QryMatch 42.3%; Pred. No. 6.06e-63;
Matches 95; Conservative 56; Mismatches 55; Indels 12; Gaps 10;

Db 2 TPWGLIVLIGSLDNGAEACTCSPHPQDAFCNSDIVIRAKVGVKLVKEGP--FGT 59
Qy 7 TRLALGLLLA-TLL-RPADACSCSPVHPQAFCNADVIRAKAVSEKVEDSGNDIYN 64

Db 60 -L--V-YTIKQMYRGFTKMPHVQYIHTASESLCGKLEVN-KYQYILTGRVY-DGKM 113
Qy 65 PIKRIQYEIKQIKMFKG-PEK-DIEFIYTPSSAVCGVSLDVGKKEVLIAGKAEKGDM 122
Db 114 YTGICNFVERWDLTSLQKGLNRYHLGCNCKIKSCYILPCFVTSKNECLWTDMLSNFG 173
Qy 123 HITLCDFIVPWDTLTSTQKSLNRYQMGCECKITRCMPICYISSPDECLMDWDWTEKN 182
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Db 174 YPGVQSKHVACIROKGYCSWYRGAPDKSIINATDP 211  
 QY 183 INGHQAKFFACIKRSGCAWYRGAPDKQEFIDIEDP 220

RESULT 9  
 ID US-08-167-463-13 STANDARD; PRT; 212 AA.  
 XX  
 AC xxxxxx  
 DT 01-JAN-1900  
 XX  
 DE Sequence 13, Application US/08167463.  
 XX  
 CC Sequence 13, Application US/08167463  
 CC GENERAL INFORMATION:  
 CC APPLICANT: HAWKES, SUSAN P.  
 CC APPLICANT: KISHNANI, NARENDRA S.  
 CC APPLICANT: YANG, TE-TUAN  
 CC TITLE OF INVENTION: HUMAN TIMP-3  
 CC NUMBER OF SEQUENCES: 32  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: MORRISON & FOERSTER  
 CC STREET: 755 Page Mill Road  
 CC CITY: Palo Alto  
 CC STATE: California  
 CC COUNTRY: USA  
 CC ZIP: 94304-1018  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/167,463  
 CC FILING DATE: 13-DEC-1993  
 CC CLASSIFICATION: 530  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: LEHNHARDT, SUSAN K.  
 CC REGISTRATION NUMBER: 33,943  
 CC REFERENCE/DOCKET NUMBER: 22000-20542.20  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: (415) 813-5600  
 CC TELEFAX: (415) 494-0792  
 CC TELEX: 706141  
 CC INFORMATION FOR SEQ ID NO: 13:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 212 amino acids  
 CC TYPE: amino acid  
 CC STRANDEDNESS: single  
 CC TOPOLOGY: linear  
 SQ SEQUENCE 212 AA; 24504 MW; 238212 CN;

DB 33; Score 686; Match 45.2%; QryMatch 41.8%; Pred. No. 5.91e-62;  
 Matches 90; Conservative 49; Mismatches 50; Indels 10; Gaps 8;

Db 22 AEACTCVPITHPOAFNCSDIVIRAKVVGKLMKDG--FGT-M-R--YTVKQMKYRGFQ 75  
 QY 24 ADACSCSPVHPQAFNCADVVIRAKAVSEKVDGNDIYGNPIKRIQYIKQIMFKG-P 82

Db 76 IMPHVQYIYTEASESLCGKLEVN-KYQYLITGRVY-EGKYVTGLCNWYKWDRLTISQR 133  
 QY 83 EK-DIEFIYITAPSSAVCGVSLDVGKKEYLIAGKAGDKMHTLCDFIYVWDTLSTQK 141

Db 134 KGLNHRHYHLGCGCKIRPCYILPCFATSKNECIWTDMLSNFGHSGHQAKHYACIORVEGYC 193  
 QY 142 KSLNHRHYOMGCEKTRPCMPICVYISSPDECLMDWVTEKNIINGHQAKFFACIKRSDGSC 201

Db 194 SWYRGWAPPDKTIINATDP 212  
 QY 202 AWYRGAPPKQEFIDIEDP 220

RESULT 10  
 ID US-08-167-463-14 STANDARD; PRT; 211 AA.  
 XX  
 AC xxxxxx  
 DT 01-JAN-1900  
 XX  
 DE Sequence 14, Application US/08167463.  
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 CC Sequence 14, Application US/08167463  
 CC GENERAL INFORMATION:  
 CC APPLICANT: HAWKES, SUSAN P.  
 CC APPLICANT: KISHNANI, NARENDRA S.  
 CC APPLICANT: YANG, TE-TUAN  
 CC TITLE OF INVENTION: HUMAN TIMP-3  
 CC NUMBER OF SEQUENCES: 32  
 CC CORRESPONDENCE ADDRESS:  
 CC ADDRESSEE: MORRISON & FOERSTER  
 CC STREET: 755 Page Mill Road  
 CC CITY: Palo Alto  
 CC STATE: California  
 CC COUNTRY: USA  
 CC ZIP: 94304-1018  
 CC COMPUTER READABLE FORM:  
 CC MEDIUM TYPE: Floppy disk  
 CC COMPUTER: IBM PC compatible  
 CC OPERATING SYSTEM: PC-DOS/MS-DOS  
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CC CURRENT APPLICATION DATA:  
 CC APPLICATION NUMBER: US/08/167,463  
 CC FILING DATE: 13-DEC-1993  
 CC CLASSIFICATION: 530  
 CC ATTORNEY/AGENT INFORMATION:  
 CC NAME: LEHNHARDT, SUSAN K.  
 CC REGISTRATION NUMBER: 33,943  
 CC REFERENCE/DOCKET NUMBER: 22000-20542.20  
 CC TELECOMMUNICATION INFORMATION:  
 CC TELEPHONE: (415) 813-5600  
 CC TELEFAX: (415) 494-0792  
 CC TELEX: 706141  
 CC INFORMATION FOR SEQ ID NO: 14:  
 CC SEQUENCE CHARACTERISTICS:  
 CC LENGTH: 211 amino acids  
 CC TYPE: amino acid  
 CC STRANDEDNESS: single  
 CC TOPOLOGY: linear  
 SQ SEQUENCE 211 AA; 24182 MW; 246088 CN;

SQ	SEQUENCE	198 AA; 22733 MW; 214743 CN;
DB 30;	Score	685; Match 44.7%; QryMatch 41.7%; Pred. No. 7.61e-62;
Matches	89;	Conservative 50; Mismatches 50; Indels 10; Gaps 8;
Dbb	8	AFACTCSPHQDAFCNSDIVIRAKVGGKLVKEGP--FGT-L--V-VYIKQMRYRCFT 61 : : : : :   : : : : :   : : : : :   : : : : :   : : : : :   : : : : :
Qy	24	ADACSCSPHPQQAFCNADVIRAKAVSEKVDSGNDIYGNP IKRIQEIYKQIRMFKG-P 82 : : : : :   : : : : :   : : : : :   : : : : :   : : : : :   : : : : :
Dbb	62	KMPHVQYIIHTASESICGLKLEVN-KYQVILLTRGVY-DCKMYTGLCNFVERMDOLITLSQR 119 : : : : :   : : : : :   : : : : :   : : : : :   : : : : :   : : : : :
Qy	83	EK-DIEFYTPASSAVCGSLDVGGRKEVLIAGKAEGDKMHIITCLDFIVFDWLTSTQK 141 : : : : :   : : : : :   : : : : :   : : : : :   : : : : :   : : : : :
Dbb	120	KGINRYRHLCGNCKIKSYILPCFVTSKNECLWTDLMSLPGYPGQSQKHAYCIROKGYC 179 : : : : :   : : : : :   : : : : :   : : : : :   : : : : :   : : : : :
Qy	142	KSINHRYQMGCCEKITRCPMIPCYISSPDECLMWDWTEKNINGHOAKFFACIKRSSDGC 201 : : : : :   : : : : :   : : : : :   : : : : :   : : : : :   : : : : :
Dbb	180	SWYRGWAPDPKSIINATDP 198 : : : : :   : : : : :   : : : : :   : : : : :   : : : : :   : : : : :
Qy	202	AWYRGAAAPPKOEFLIEDFP 220 : : : : :   : : : : :   : : : : :   : : : : :   : : : : :   : : : : :

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RESULT 12
ID PCT-US94-11241-15 STANDARD; 198 AA.
XX
XX AC
XX AC
XX DT 01-JAN-1900
XX
XX DE Sequence 15, Application PC/TUS9411241.
XX DE
XX DE Sequence 15, Application PC/TUS9411241
XX DE GENERAL INFORMATION:
XX CC APPLICANT: Silbiger, Scott M.
XX CC APPLICANT: Koski, Raymond A.
XX CC TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
XX CC TITLE OF INVENTION: Three (TIMP-3) Composition and Methods
XX CC NUMBER OF SEQUENCES: 21
XX CC CORRESPONDENCE ADDRESS:
XX CC ADDRESSEE: Amgen Inc./Patent Operations/KMP
XX CC STREET: 1840 Dehavilland Drive
XX CC CITY: Thousand Oaks
XX CC STATE: California
XX CC COUNTRY: USA
XX CC ZIP: 91320-1789
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC COMPUTER: IBM PC compatible
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
XX CC SOFTWARE: PatentIn Release #1.0, Version #1.25
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: PCT/US94/11241
XX CC FILING DATE:
XX CC CLASSIFICATION:
XX CC INFORMATION FOR SEQ ID NO: 15:
XX CC SEQUENCE CHARACTERISTICS:
XX CC LENGTH: 198 amino acids
XX CC TYPE: amino acid
XX CC STRANDEDNESS: single
XX CC TOPOLOGY: linear

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RESULT 12
ID PCT-US94-11241-15 STANDARD; 198 AA.
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XX xxxxxx
XX 01-JAN-1900
XX
XX DE Sequence 15, Application PC/TUS9411241.
XX
XX DE Sequence 15, Application PC/TUS9411241
XX GENERAL INFORMATION:
XX APPLICANT: Silbiger, Scott M.
XX APPLICANT: Koski, Raymond A.
XX TITLE OF INVENTION: Tissue Inhibitor Metalloprotease
XX TITLE OF INVENTION: Three (TIMP-3) Composition and
XX NUMBER OF SEQUENCES: 21
XX CORRESPONDENCE ADDRESS:
XX ADDRESSEE: Amgen Inc./Patent Operations/KMP
XX STREET: 1840 Dehavilland Drive
XX CITY: Thousand Oaks
XX STATE: California
XX COUNTRY: USA
XX ZIP: 91320-1789
XX
XX COMPUTER READABLE FORM:
XX MEDIUM TYPE: Floppy disk
XX COMPUTER: IBM PC compatible
XX OPERATING SYSTEM: PC-DOS/MS-DOS
XX SOFTWARE: PatentIn Release #1.0, Version #1.25
XX CURRENT APPLICATION DATA:
XX APPLICATION NUMBER: PCT/US94/11241
XX FILING DATE:
XX CLASSIFICATION:
XX INFORMATION FOR SEQ ID NO: 15:
XX SEQUENCE CHARACTERISTICS:
XX LENGTH: 198 amino acids
XX TYPE: amino acid
XX STRANDEDNESS: single
XX TOPOLOGY: linear
XX

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CC MOLECULE TYPE: protein  
SQ SEQUENCE 198 AA; 22733 MW; 214743 CN;  
DB 4; Score 685; Match 44.7%; QryMatch 41.7%; Pred. No. 7.61e-62;  
Matches 89; Conservative 50; Mismatches 50; Indels 10; Gaps 8;  
Db 8 AEACTSPSPHQAFCNSDIVIRAKVVGKLVKEGP--FGT-L--V-YTIKQMYRGFT 61  
Qy 24 ADACSPVHPQAFQCNADVIRAKAVSEKVDGNDIYGNPIKRIQYIKQIKFKG-P 82  
Db 62 KPHVQVIHTAESESLGGLKLEVN-KYQYLITGRVY-DGRMYTGLCNFVERWDQILTSQR 119  
Qy 83 EK-DIEFIYAPSSAVCGVSLDVGGKKEYLIAGKAGDGKMHITLCDFIVPMDLSTTQK 141  
Db 120 KGLNRYHLGCNCKIKSCYLLPCFVTSKNECLWTDMLSNFGVPGVQSKHYACIRKGGYC 179  
Qy 142 KSLNRYQMGCEKITRCMPICYISSPDECLWMDWTEKNINGHOAKFFACIKRSDGSC 201  
Db 180 SWYRGWAPPDKSIINATDP 198  
Qy 202 AWYGAAPPKQEFIDIEDP 220  
RESULT 13  
ID US-08-167-463-1 STANDARD; PRT; 188 AA.  
XX  
AC xxxxxx  
XX  
DT 01-JAN-1900  
XX  
DE Sequence 1, Application US/08167463.  
CC Sequence 1, Application US/08167463  
CC GENERAL INFORMATION:  
CC APPLICANT: HAWKES, SUSAN P.  
CC APPLICANT: KISHNANI, NARENDRA S.  
CC APPLICANT: YANG, TE-TUAN  
CC TITLE OF INVENTION: HUMAN TIMP-3  
CC NUMBER OF SEQUENCES: 32  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: MORRISON & FOERSTER  
CC STREET: 755 Page Mill Road  
CC CITY: Palo Alto  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 94304-1018  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/167,463  
CC FILING DATE: 13-DEC-1993  
CC CLASSIFICATION: 530  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: LEHNHARDT, SUSAN K.  
CC REGISTRATION NUMBER: 33,943  
CC REFERENCE/DOCKET NUMBER: 22000-20542.20  
CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (415) 813-5600  
CC TELEFAX: (415) 494-0792  
CC TELEX: 706141  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 188 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
SQ SEQUENCE 188 AA; 21822 MW; 186841 CN;  
DB 33; Score 673; Match 44.9%; QryMatch 41.0%; Pred. No. 1.58e-60;  
Matches 88; Conservative 48; Mismatches 50; Indels 10; Gaps 8;  
Db 1 CTCVPHPQDAFNCSDIVIRAKVVGKLMKDG--FGT-M-R--YTVKQMYRGFTQIMP 54  
Qy 27 CSCPVPHPQAFQCNADVIRAKAVSEKVDGNDIYGNPIKRIQYIKQIKFKG-PEK- 84  
Db 55 HVQYIYTEASESLGCVKLEVN-KYQYLITGRVY-EKQVYTGICNWEKWDRLTSLORKGL 112  
Qy 85 DIEFIYAPSSAVCGVSLDVGGKKEYLIAGKAGDGKMHITLCDFIVPMDLSTTQKSL 144  
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RESULT 14  
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AC xxxxxx  
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DT 01-JAN-1900  
XX  
DE Sequence 17, Application US/08134231.  
CC Sequence 17, Application US/08134231  
CC GENERAL INFORMATION:  
CC APPLICANT: Silbiger, Scott M.  
CC APPLICANT: Koski, Raymond A.  
CC TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type  
CC TITLE OF INVENTION: Three (TIMP-3) Composition and Methods  
CC NUMBER OF SEQUENCES: 21  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Angen Inc./Patent Operations/RMP  
CC STREET: 1840 Dehavilland Drive  
CC CITY: Thousand Oaks  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 91320-1789  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/167,463  
CC FILING DATE: 13-DEC-1993  
CC CLASSIFICATION: 530  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: LEHNHARDT, SUSAN K.  
CC REGISTRATION NUMBER: 33,943  
CC REFERENCE/DOCKET NUMBER: 22000-20542.20  
CC TELECOMMUNICATION INFORMATION:



1 ann1  
2 ann2  
3 ann3  
4 unann1  
5 unann2  
6 unann3  
7 unann4  
8 unann5  
9 unann6  
10 unann7  
11 unann8  
12 unrev1  
13 unrev2

Statistics: Mean 42.711; Variance 87.125; scale 0.490

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %	Length	DB	ID	Description	Pred. No.
1	1643	100.0	220	4	A37128	metalloproteinase ti	0.00e+00
2	1630	99.2	220	13	S45683	metalloproteinases-2	2.89e-303
3	1620	98.6	220	4	JH0683	metalloproteinase in	3.44e-301
4	1550	94.3	220	4	A35996	metalloproteinase in	1.14e-286
5	1466	89.2	196	4	S38624	metaro proteinase in	2.88e-269
6	1392	84.7	185	4	S21303	metalloproteinase in	5.84e-254
7	695	42.3	211	10	S45317	metalloproteinase ti	1.44e-111
8	686	41.8	212	10	A34329	metalloproteinase in	9.19e-110
9	686	41.8	211	11	A35352	tissue inhibitor of	9.19e-110
10	686	41.8	211	11	S43052	metalloproteinase-3	9.19e-110
11	680	41.4	210	10	S47041	mig protein - human	1.46e-108
12	677	41.2	198	11	S43053	metalloproteinase-3	5.82e-108
13	676	41.1	197	11	A49614	tissue inhibitor of	9.23e-108
14	521	31.7	207	2	ZYHUEP	metalloproteinase ti	5.23e-77
15	518	31.5	206	4	A33350	metalloproteinase in	2.03e-76
16	517	31.5	207	4	A35685	metalloproteinase in	3.19e-76
17	508	30.9	217	13	JC2557	metalloproteinase 1	1.86e-74
18	506	30.8	205	4	A26106	collagenase inhibito	4.57e-74
19	488	29.7	207	4	A26633	metalloproteinase in	1.51e-70
20	186	11.3	57	10	A39043	21K extracellular ma	1.56e-14
21	172	10.5	31	4	S18428	metalloproteinase in	3.20e-12
22	164	10.0	22	13	S20325	metalloproteinase in	6.35e-11
23	138	8.4	22	13	S20326	metalloproteinase in	7.42e-07
24	122	7.4	21	4	B39120	30K metalloproteinase	1.71e-04
25	117	7.1	290	7	S15198	hydrogenase isozyme	8.78e-04
26	100	6.1	76	11	S25146	CD24 protein - rat	1.74e-01
27	99	6.0	697	7	A26132	gag-abl-pol polyprot	2.34e-01
28	98	6.0	1025	9	S42507	probable membrane pr	3.14e-01
29	96	5.8	141	13	S15785	heat-stable antigen	5.63e-01
30	96	5.8	76	13	S15784	heat-stable antigen	5.63e-01
31	96	5.8	76	11	S43709	heat-stable antigen	5.63e-01
32	96	5.8	76	11	A43537	heat-stable antigen	5.63e-01
33	96	5.8	76	11	S43129	heat-stable antigen	5.63e-01
34	93	5.7	310	10	S53717	dlk protein - human	1.33e+00
35	93	5.7	404	7	B45313	putrescine transport	1.33e+00

36 93 5.7 383 10 B45484 delta-like dlk homeo 1.33e+00  
37 91 5.5 206 3 NBH01B platelet glycoprotei 2.33e+00  
38 91 5.5 3033 3 GNVJ18 genome polyprotein - 2.33e+00  
39 90 5.5 806 6 A46271 integrin beta P, int 3.08e+00  
40 90 5.5 26 4 A48417 gelatinase, 96K - hu 3.08e+00  
41 90 5.5 805 6 A42483 integrin beta-7 chain 3.08e+00  
42 90 5.5 806 6 B46503 beta 7 integrin=lymp 3.08e+00  
43 89 5.4 361 11 A53860 chondroaderin precu 4.06e+00  
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## ALIGNMENTS

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DATE 08-Mar-1991 #sequence\_revision 08-Mar-1991 #text\_change 05-Apr-1995  
ACCESSIONS A37128; B35996; A34464; A34415  
REFERENCE A37128  
#authors Stetler-Stevenson, W.G.; Brown, P.D.; Onisto, M.; Levy, A.T.; Liotta, L.A.  
#journal J. Biol. Chem. (1990) 265:13933-13938  
#title Tissue inhibitor of metalloproteinases-2 (TIMP-2) mRNA  
#cross-references MUID:90338014  
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REFERENCE A35996  
#authors Boone, T.C.; Johnson, M.J.; De Clerck, Y.A.; Langley, K.E.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2800-2804  
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#authors Stetler-Stevenson, W.G.; Kruttsch, H.C.; Liotta, L.A.  
#journal J. Biol. Chem. (1989) 264:17374-17378  
#title Tissue inhibitor of metalloproteinase (TIMP-2). A new member of the metalloproteinase inhibitor family.  
#cross-references MUID:90008902  
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REFERENCE A34415  
#authors Goldberg, G.I.; Marmer, B.L.; Grant, G.A.; Eisen, A.Z.; Wilhelm, S.; He, C.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:8207-8211  
#title Human 72-kilodalton type IV collagenase forms a complex with a tissue inhibitor of metalloproteinases designated TIMP-2.  
#cross-references MUID:90046765  
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KEYWORDS extracellular protein; proteinase inhibitor
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Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 121 kmhitcdfiwpdltstqkkslnhryqmgceckitrcpmipcyispedclmwdwvte 180
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ORGANISM #formal name Rattus norvegicus #common name Norway rat
DATE 10-Dec-1994 #sequence_revision 10-Dec-1994 #text_change
10-Dec-1994
ACCESSIONS S45683
REFERENCE #authors Cook, T.F.; Burke, J.S.; Bergman, K.D.; Quinn, C.O.; Jeffrey,
J.J.; Partridge, N.C.
#journal Arch. Biochem. Biophys. (1994) 311:313-320
#title Cloning and regulation of rat tissue inhibitor of
metalloproteinases-2 in osteoblastic cells.
#accession S45683
#status preliminary
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ORGANISM #formal name Mus musculus #common name house mouse
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
28-Apr-1995
ACCESSIONS JH0683; JCI234; S26189
REFERENCE #authors Shimizu, S.; Malik, K.; Sejima, H.; Kishi, J.; Hayakawa, T.;
Koizumi, O.
#journal Gene (1992) 114:291-292
#title Cloning and sequencing of the cDNA encoding a mouse tissue
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#accession JH0683
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#cross-references EMBL:X62622
#experimental source 3T3 fibroblast, strain Balb/c
REFERENCE JCI234
#authors Leco, K.J.; Hayden, L.J.; Sharma, R.R.; Rocheleau, H.;
Greenberg, A.H.; Edwards, D.R.
#journal Gene (1992) 117:209-217
#title Differential regulation of TIMP-1 and TIMP-2 mRNA expression
in normal and Ha-ras-transformed murine fibroblasts.
#cross-references MUID:92347695
#accession JCI234
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FEATURE
1-26 #domain signal sequence #status predicted #label SIG\
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SUMMARY #length 220 #molecular-weight 24328 #checksum 6045
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Db 121 kmhltcdvfpwdtltsttkkslnhrygmgeckitrcpmipcyispsdeclwmdwvte 180  
Qy 121 kmhltcdvfpwdtltsttkkslnhrygmgeckitrcpmipcyispsdeclwmdwvte 180  
Db 181 kslngqakffacikrsdgscaawyrgaapppkqefldiedp 220  
Qy 181 kslngqakffacikrsdgscaawyrgaapppkqefldiedp 220

RESULT 4  
ENTRY A35996 #type complete  
TITLE metalloproteinase inhibitor 2 precursor - bovine  
ALTERNATE\_NAMES collagenase inhibitor; tissue inhibitor of metalloproteinases (TIMP-2)  
ORGANISM #formal name Bos primigenius taurus #common name cattle  
DATE 16-Nov-1990 #sequence\_revision 16-Nov-1990 #text\_change 05-Apr-1995  
ACCESSIONS A35996; A34468; A25322; S28151  
REFERENCE A35996  
#authors Boone, T.C.; Johnson, M.J.; De Clerck, Y.A.; Langley, K.E.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:2800-2804  
#title cDNA cloning and expression of a metalloproteinase inhibitor related to tissue inhibitor of metalloproteinases.  
#cross-references MUID:90207285  
#accession A35996  
##molecule\_type mRNA  
##residues 1-220 #label B00  
##cross-references GB:M2303  
##experimental\_source aortic endothelium  
REFERENCE A34468  
#authors De Clerck, Y.A.; Yean, T.D.; Ratzkin, B.J.; Lu, H.S.; Langley, K.E.  
#journal J. Biol. Chem. (1989) 264:17445-17453  
#title Purification and characterization of two related but distinct metalloproteinase inhibitors secreted by bovine aortic endothelial cells.  
#cross-references MUID:90008914  
#accession A34468  
##status preliminary  
##molecule\_type protein  
##residues 27-71 #label DEC  
REFERENCE A25322  
#authors Murray, J.B.; Allison, K.; Sudhalter, J.; Langer, R.  
#journal J. Biol. Chem. (1986) 261:4154-4159  
#title Purification and partial amino acid sequence of a bovine cartilage-derived collagenase inhibitor.  
#cross-references MUID:86140235  
#accession A25322  
##molecule\_type protein  
##residues 27-41, 'C', 43-55, 'EX', 58-59, 'X', 61-66, 'XS', 69-71 #label MUR  
##experimental\_source cartilage  
REFERENCE S28151  
#authors DeClerck, Y.A.; Yean, T.D.; Lee, Y.; Tomich, J.M.; Langley, K.E.  
#journal Biochem. J. (1993) 289:65-69  
#title Characterization of the functional domain of tissue inhibitor of metalloproteinases-2 (TIMP-2).  
#contents annotation; functional domain  
CLASSIFICATION #superfamily metalloproteinase inhibitor

KEYWORDS proteinase inhibitor  
FEATURE #domain signal sequence #status predicted #label SIG\  
1-26 #product metalloproteinase inhibitor 2 #status predicted  
27-220 #label MAT\  
27-158 #region inhibitory #status predicted  
SUMMARY #length 220 #molecular-weight 24355 #checksum 3345

DB 4; Score 1550; Match 91.8%; QryMatch 94.3%; Pred. No. 1.14e-286; Matches 202; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Db 1 mqaarslplafcllltllptadacspvhpqqafcnadivirakvnnkveadsgnd 60  
Qy 1 mqaarturlalglullatllrpdadcsfpvhpqqafcnadivirakvnnkveadsgnd 60  
Db 61 iygnpikriqveikqkmgkpgdgdiefiytapaavcgvsldvggkkeyliagkaegnd 120  
Qy 61 iygnpikriqveikqkmgkpgdgdiefiytapaavcgvsldvggkkeyliagkaegnd 120  
Db 121 nmhltcdvfpwdtltsttkkslnhrygmgeckitrcpmipcyispsdeclwmdwvte 180  
Qy 121 kmhltcdvfpwdtltsttkkslnhrygmgeckitrcpmipcyispsdeclwmdwvte 180  
Db 181 kninghqakffacikrsdgscaawyrgaapppkqefldiedp 220  
Qy 181 kninghqakffacikrsdgscaawyrgaapppkqefldiedp 220

RESULT 5  
ENTRY S38624 #type fragment  
TITLE metaro proteinase inhibitor, tissue - Chinese hamster (fragment)  
ORGANISM #formal name Cricetulus griseus #common name Chinese hamster  
DATE 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 12-Apr-1995  
ACCESSIONS S38624  
REFERENCE S38624  
#authors Suzuki, Y.  
#submission submitted to the EMBL Data Library, November 1993  
#accession S38624  
##status preliminary  
##molecule\_type mRNA  
##residues 1-196 #label S02  
##cross-references EMBL:X75924  
CLASSIFICATION #superfamily metalloproteinase inhibitor  
SUMMARY #length 196 #checksum 7766

DB 4; Score 1466; Match 99.0%; QryMatch 89.2%; Pred. No. 2.88e-269; Matches 193; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 2 acscspvhpqgafcnadivirakavsekdsgndiynpikriqveikqkmgkpgdkd 61  
Qy 26 acscspvhpqgafcnadivirakavsekdsgndiynpikriqveikqkmgkpgdkd 85  
Db 62 lefiytpassavcgvsldvggkkeyliagkaegdkmhltcdvfpwdtltsttkksln 121  
Qy 86 lefiytpassavcgvsldvggkkeyliagkaegdkmhltcdvfpwdtltsttkksln 145  
Db 122 hrygmgeckitrcpmipcyispsdeclwmdwvteknghqakffacikrsdgscaawy 191

```
QY 146 HRYOMGCECKITRCMPICVYISSPDECLWMDVWTEKNGHOAKFFACIKRSDGSCAWYR 205
Db 182 gaappkqefldiedp 196
QY 206 GAAPPKQEFLDIEDP 220

RESULT 6 S21303 #type fragment
ENTRY metalloproteinase inhibitor 2, tissue - human (fragment)
TITLE #formal name Homo sapiens #common name man
ORGANISM 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
DATE 12-Apr-1995

ACCESSIONS S21303
REFERENCE S21303
#authors Malik, K.; Sejima, H.; Aoki, T.; Iwata, K.
#submission submitted to the EMBL Data Library, August 1990
#description Nucleotide sequence of a TIMP-II cDNA.
#accession S21303

##status preliminary
##molecule_type mRNA
##residues 1-185 ##label MAL
##cross-references EMBL:X54533
CLASSIFICATION #superfamily metalloproteinase inhibitor
SUMMARY #length 185 #checksum 2530

Db 4; Score 1392; Match 99.5%; QryMatch 84.7%; Pred. No. 5.84e-254;
Matches 184; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 spvhpqafcnadvirakavsekevdsgndiynpikriyveikqkfmfgpekdiefi 60
QY 30 SPVHPQOAFCNADVIRAKAVSEKEVDSGNDIYNPIKRIQVEIKQKFMFGPEKDIEFI 89

Db 61 ytapssvqgvaldvqgkkeyliagkaeqdgknhitlcfvvpwdtltatgkkslnhryq 120
QY 90 YTAPSSAVCGVSLDVGGKKEYLIAGKAEDGKMHITLDCFIVPMDTTLSTQKKSINHRYQ 149

Db 121 mgceckitrcmpicvyspdeclwmdvteknghqakffacikrdsdcawyr gaap 180
QY 150 MGCECKITRCMPICVYISSPDECLWMDVWTEKNGHOAKFFACIKRSDGSCAWYRGAAP 209

Db 181 pkqef 185
QY 210 PKQEF 214

RESULT 7 S45317 #type complete
ENTRY metalloproteinase tissue inhibitor 3 - human
TITLE #formal name Homo sapiens #common name man
ORGANISM 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
DATE 03-Mar-1995

ACCESSIONS S45317
REFERENCE S45317
#authors Uria, J.A.; Ferrando, A.A.; Velasco, G.; Freije, J.M.P.;
#journal Lopez-Otin, C.
#journal Cancer Res. (1994) 54:2091-2094
#title Structure and expression in breast tumors of human TIMP-3, a
#accession S45317 new member of the metalloproteinase inhibitor family.
```

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##status preliminary
##molecule_type mRNA
##residues 1-211 ##label URI
##cross-references EMBL:X76227
SUMMARY #length 211 #molecular-weight 24145 #checksum 4550

Db 10; Score 695; Match 43.6%; QryMatch 42.3%; Pred. No. 1.44e-111;
Matches 95; Conservative 56; Mismatches 55; Indels 12; Gaps 10;

Db 2 tpwlgilvlgswalgdgaectspshpdafofnsdivirakvvgkklvkegp---fgt 59
QY 7 TIRLALGILLILA-TLL-RPADACSCSPVHPQOAFCNADVIRAKAVSEKEVDSCNDIYGN 64

Db 60 l--v-ytikmqmrygrftkmpvhyihteaaseslqgkllevn-kyqyllitgrvy-dgkm 113
QY 65 PIKRIQVEIKQKFMFG--PEK-DIEFIYTPASSAVCGVSLDVGGKKEYLIAGKAEDGKGM 122

Db 114 ytgicnfverwdqtltsqrkglvnyrhlgcncikscyyilpcfvtskneclwdmlsnfg 173
QY 123 HITLCLDFIVPMDTTLSTQKKSINHRYOMGCECKITRCMPICVYISSPDECLWMDVWTEKN 182

Db 174 ypgvqskhyacirqkgycswyrgwappdksiinatdp 211
QY 183 INGHQAKFFACIKRSDGSCAWYRGAAPPKQEFLDIEDP 220

RESULT 8 A43429 #type complete
ENTRY metalloproteinase inhibitor CHIMP-3 - chicken
TITLE #formal name Gallus gallus #common name chicken
ORGANISM 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
DATE 11-Apr-1995

ACCESSIONS A43429
REFERENCE A43429
#authors Pavloff, N.; Staskus, P.W.; Kishnani, N.S.; Hawkes, S.P.
#journal J. Biol. Chem. (1992) 267:17321-17326
#title A new inhibitor of metalloproteinases from chicken: CHIMP-3.
#cross-references MIM:92381050
#accession A43429

##status preliminary
##molecule_type mRNA
##residues 1-212 ##label PAV
##cross-references NCBI:111960; NCBI:111961
##experimental_source embryo
##note #length 212 #molecular-weight 24504 #checksum 6267
SUMMARY

Db 10; Score 686; Match 45.2%; QryMatch 41.8%; Pred. No. 9.19e-110;
Matches 90; Conservative 49; Mismatches 50; Indels 10; Gaps 8;

Db 22 aeactcvpihpqdafofnsdivirakvvgkklmkdgp---fgt-m-r--ytvqgmkmvrgfq 75
QY 24 ADACSCSPVHPQOAFCNADVIRAKAVSEKEVDSGNDIYNPIKRIQVEIKQKFMFG--P 82

Db 76 imphvqvlyiteaseslqgkkllevn-kyqyllitgrvy-egkvtyglcnwyekwdrlttsqr 133
QY 83 EK-DIEFIYTPASSAVCGVSLDVGGKKEYLIAGKAEDGKMHITLCLDFIVPMDTTLSTQK 141

Db 134 kglhryhlgcgckirpcyylpcfatekneclwtmnlsgnfhghqakhyaciqrvegyc 193
```

```

Db 194 swyrgwapdktiinatdp 212
      :||| ||| :: ||
QY 202 AWYRGAPPKQEFLDIEDP 220

```

ACCESSIONS  
A53532  
REFERENCE  
#authors  
Leco, K.J.; Khokha, R.; Pavloff, N.; Hawkes, S.P.; Edwards,  
D.R.

```
#accession A53532 preliminary
#status
#molecule_type mRNA
#residues 1-211 #label LEC
#cross-references GR:127424
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DB 11; Score 686; Match 43.1%; QryMatch 41.8%; Pred. No. 9.19e-110; Matches 99; Conservative 56; Mismatches 56; Indels 12; Gaps 10;

[illegible]

Db	174	yggygskhyacirkggygcywrgwappdksi	natdp	211
		:   :   :   :   :   :   :   :		
QV	183	INGHQAFTACIKRSDGSCAWYGAAPPKQFF	LDIEDP	220

RESULT	10
ENTRY	S43052
TITLE	#type complete metalloproteinase-3 tissue inhibitor - mouse
ORGANISM	#formal name Mus musculus #common name house mouse
DATE	06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
ACCESSIONS	S43052
REFERENCE	S43052

#cross references	20079
#length	211
#molecular-weight	24182
#checksum	4940

SUMMARY

Db 2 tptwlgvlvllscwslghwgaeeactcspshpqpdaefcnsdivirakvwgkklvkegp--fgt 59

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Db 60 -l--vtikmqmrygfskmpbhvqylhteaseslclglevn-kyqylltgrvy-egkm 11
      :  :  |||:||||:  :  :||:  :  :||:  :  :||:  :  :||:  :  :||:  :  :||:
      :  :  |||:||||:  :  :||:  :  :||:  :  :||:  :  :||:  :  :||:  :  :||:
```

```

114 ytglnfverwdhltlsqrkglnryhlgcncikscyylpcfvtskneclwtcdmlsnfg 17
      |||: || |:|:| |||:| ||| | |||:| ||| | |||:| ||| | |||:|
123 HITLCDFVWDITSTOKKSLNHRVQMGCECKITRCPMIPCYISSDECINWDVWTEKN 18

```

183 INGHOAFFACIKRSDGSCAWYRGAAAPKOEFLDIDP 220

ENTRY	S47041	#type complete
TITLE	mg protein - human	
ORGANISM	#formal name Homo sapiens	
DATE	20-Feb-1995	#sequence rev 20-Feb-1995

#submission submitted to the EMBL Data Library, February 1994  
#description A novel member of the TMP gene family is regulated during G1 progression, mitogenic stimulation, differentiation and senescence.

##cross-references EMBL:Z30183

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Db      5 lglvllgswsgwgagprctcspshpqdafncsdvirakvvgklykegp--fgt-l-- 59
       |||:||:: :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :| | :| :|
Ov     12 lgu-lIATII RPADA--CSCSPVHPQAAFCNADWIRAKVSEKVD SGNDYGNPIKR 68
```

60 v-ytikmkmvrgftkmpghvyibteaseslclgikievn-kygyvlltrgwy-dgkmytql 11  
69 IYEYIKQKMFKG-PEK-DIFITYAPSSAVCGVSDVGGKEYYLLAGRAEGDGRHHTL 12  
Db QV

Db	117	cnfverwdqltlsqrklnryrhlgcnckikscyylpcfvtskneclwtmdlnsfgyppg	176	
Qy	127	CDFIVPMDTLSTQKSLNHYQMGCEKITRCFMPICYSISPDCECLMDWVTEKNIHG	186	
Db	177	qskhyacirkggycswrgwappkksinatdp	210	
Qy	187	QAKFFACIKRSDGSCAWYRGAAPRQEFIDIEDP	220	
RESULT	12			
ENTRY		S43053	#type complete	
TITLE		metalloproteinase-3 tissue inhibitor - mouse		
ORGANISM		#formal_name Mus musculus #common name mouse		
DATE		13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change		
ACCESSIONS		S43053		
REFERENCE		S43053		
#authors		Sun, Y.; Hegamyer, G.; Colburn, N.H.		
#journal		Cancer Res. (1994) 54:1139-1144		
#title		Molecular cloning of five messenger RNAs differentially expressed in preneoplastic or neoplastic JB6 mouse epidermal cells: one is homologous to human tissue inhibitor of metalloproteinase-3.		
#accession		S43053		
#status		preliminary		
#molecule_type		DNA		
#residues		1-198 #label SUN		
#cross-references		EMBL:230970		
SUMMARY		#length 198 #molecular-weight 22768 #checksum 1889		
Db	111	Score	677; Match 44.2%; QryMatch 41.2%; Pred. No. 5.82e-108;	
Matches		88; Conservative	51; Mismatches 50; Indels 10; Gaps 8;	
Db	8	aeactcspshpqdafcnslvirakvvgklvkpg--fgt-l--v-ytikgmkyrgfs	61	
Qy	24	ADACSCSPVHPQQAFCNADVVIRAKAVSEKVDGNDIYGNPKRIQYIKQIKMFKG-P	82	
Db	62	kphvqyhteaseslclgklevn-Kyqylltgrvy-ekgmytgcfnfverwdhtlsqr	119	
Qy	83	EK-DIEFIYTPASSAVCGSLDVGGKKEYLIAGKAECDGKMHITLCDFIVPMDTLSTQK	141	
Db	120	kqlnryhlgcnckikscyylpcfvtskneclwtmdlnsfgyppgqskhyacirkgyc	179	
Qy	142	KSLNHYQMGCEKITRCFMPICYSISPDCECLMDWVTEKNIHGQAKFFACIKRSDGSC	201	
Db	180	swrgwappkksinatdp	198	
Qy	202	AWYRGAAPKQEFIDIEDP	220	
RESULT	13			
ENTRY		A49614	#type fragment	
TITLE		tissue inhibitor of metalloproteinase 3 - human (fragment)		
ORGANISM		#formal_name Homo sapiens #common name man		
DATE		20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change		
ACCESSIONS		A49614		
REFERENCE		A49614		
#authors		Apte, S.S.; Mattei, M.G.; Olsen, B.R.		
#journal		Genomics (1994) 19:86-90		
#title		Cloning of the cDNA encoding human tissue inhibitor of metalloproteinase-3 (TIMP-3) and mapping of the TIMP3 gene to chromosome 22.		
#accession		A49614		
#status		preliminary		
#molecule_type		mRNA		
#residues		1-197 #label APT		
#cross-references		GB:L15073		
GENETICS				
#gene		GDB:TIMP3		
SUMMARY		#length 197 #checksum 677		
Db	111	Score	676; Match 44.7%; QryMatch 41.1%; Pred. No. 9.23e-108;	
Matches		88; Conservative	49; Mismatches 50; Indels 10; Gaps 8;	
Db	9	actcspshpqdafcnslvirakvvgklvkpg--fgt-l--v-ytikgmkyrgftkm	62	
Qy	26	ACSCSPVHPQQAFCNADVVIRAKAVSEKVDGNDIYGNPKRIQYIKQIKMFKG-PEK	84	
Db	63	phvqyhteaseslclgklevn-Kyqylltgrvy-dgkmytgcfnfverwdhtlsqrk	120	
Qy	85	-DIEFIYTPASSAVCGSLDVGGKKEYLIAGKAECDGKMHITLCDFIVPMDTLSTQKKS	143	
Db	121	lnryhlgcnckikscyylpcfvtskneclwtmdlnsfgyppgqskhyacirkgycsw	180	
Qy	144	LNHRYQMGCEKITRCFMPICYSISPDCECLMDWVTEKNIHGQAKFFACIKRSDGSCAW	203	
Db	181	yrqwapdkksinatdp	197	
Qy	204	YRGAAPKQEFIDIEDP	220	
RESULT	14			
ENTRY		ZYHUEP	#type complete	
TITLE		metalloproteinase tissue inhibitor 1 precursor - human		
ALTERNATE_NAMES		erythroid potentiating activity (EPA); fibroblast collagenase inhibitor; tissue inhibitor of metalloproteinases (TIMP)		
ORGANISM		#formal_name Homo sapiens #common name man		
DATE		28-May-1986 #sequence_revision 28-May-1986 #text_change		
ACCESSIONS		A93372; A93363; A23534; A20595; A35826; A01269		
REFERENCE		A93372		
#authors		Docherty, A.J.P.; Lyons, A.; Smith, B.J.; Wright, E.M.; Stephens, P.E.; Harris, T.J.R.; Murphy, G.; Reynolds, J.J.		
#journal		Nature (1985) 318:66-69		
#title		Sequence of human tissue inhibitor of metalloproteinases and its identity to erythroid-potentiating activity.		
#cross-references		MUID:86040463		
#accession		A93372		
#molecule_type		mRNA		
#residues		1-207 #label DOC		
REFERENCE		A93363		
#authors		Gasson, J.C.; Golde, D.W.; Kaufman, S.E.; Westbrook, C.A.; Hewick, R.M.; Kaufman, R.J.; Wong, G.G.; Temple, P.A.; Leary, A.C.; Brown, E.L.; Orr, E.C.; Clark, S.C.		
#journal		Nature (1985) 315:768-771		
#title		Molecular characterization and expression of the gene encoding human erythroid-potentiating activity.		
#cross-references		MUID:85240567		

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#accession A93363
##molecule_type mRNA
##residues 1-207 ##label GAS
REFERENCE A23534
#authors Carmichael, D.F.; Sommer, A.; Thompson, R.C.; Anderson, D.C.;
Smith, C.G.; Welgus, H.G.; Stricklin, G.P.
#journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:2407-2411
#title Primary structure and cDNA cloning of human fibroblast
collagenase inhibitor.
#cross-references MUID:86205964
#accession A23534
##molecule_type mRNA
##residues 1-207 ##label CAR
##note parts of this sequence were confirmed by protein
sequencing
##note carbohydrate binding sites were determined
REFERENCE A20595
#authors Stricklin, G.P.; Welgus, H.G.
#journal J. Biol. Chem. (1983) 258:12252-12258
#title Human skin fibroblast collagenase inhibitor.
#cross-references MUID:84032401
#accession A20595
##molecule_type protein
##residues 24-44,'L',46 ##label STR
##note six disulfide bonds are present
REFERENCE A35826
#authors Rapp, G.; Freudenstein, J.; Klaudiny, J.; Mucha, J.; Wempe,
F.; Zimmer, M.; Scheit, K.H.
#journal DNA Cell Biol. (1990) 9:479-485
#title Characterization of three abundant mRNAs from human ovarian
granulosa cells.
#cross-references MUID:91025550
#accession A35826
##molecule_type mRNA
##residues 1-207 ##label RAP
##cross-references GB:M38188
COMMENT This protein, found in a variety of body fluids, complexes with
metalloproteinases, irreversibly inactivating them. It also
mediates erythropoiesis in vitro; but, unlike IL-3, it is
species-specific, stimulating the growth and differentiation of
only human and murine erythroid progenitors.
The remarkable heat stability of this protein may be due to
disulfide bond formation.
GENETICS
#gene GDB:TIMP1; CLGI; TIMP
#map_position Xp11.3-p11.23
CLASSIFICATION #superfamily metalloproteinase inhibitor
erythropoiesis; glycoprotein; proteinase inhibitor
FEATURE
1-23 #domain signal sequence #status predicted #label SIG\
24-207 #product metalloproteinase inhibitor #status predicted
#label MAT\
53,101 #binding site carbohydrate (Asn) (covalent) #status
experimental
SUMMARY #length 207 #molecular-weight 23171 #checksum 9750
DB 2; Score 521; Match 41.1%; QryMatch 31.7%; Pred. No. 5.23e-77;
Matches 81; Conservative 39; Mismatches 70; Indels 7; Gaps 7;
Db 7 lasgillllwlapractcvphqtafcnsdlvirakfvgtpevngtt-lvqryeikm 65

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Qy	10	LALGILLATLRPADACSPVHPQAFCNADWVRARAKVSEKVDSGNDIYGN-PIKR 68
Dd	66	tk-mykfgqal-gdaadirfvtvtpamesvcgythrshnrseeflagklq-dgllhhctc 122
Qy	69	IQYEIKQIKMPKGPEKDIEFIYTAPSSAVCGVSLDVGGKKE-YLIAGRAEGDGKMHITLC 127
Dd	123	sfvapwnslsqrrgfktytvgceectvfpcslspcklqsghclwtdqlggsekpf 182
Qy	128	DFIVPMDTLSTTKQSILNHRVQMCE-CKITRCFMPICYSIPSDDECLMWDWTEKNINGH 186
Dd	183	qsrhiacilprepdlctw 199
Qy	187	OAKFFACIKRSDGSCAW 203
RESULT	15	
ENTRY	A33350	#type complete
TITLE	metalloproteinase inhibitor - rabbit	
ORGANISM	#formal name Oryctolagus cuniculus #common_name domestic rabbit	
DATE	30-Jun-1992	#sequence_revision 30-Jun-1992 #text_change 18-Jun-1993
ACESSIONS	A33350; A30864	
REFERENCE	A33350	
#authors	Horowitz, S.; Dafni, N.; Shapiro, D.L.; Holm, B.A.; Notter, R.H.; Quible, D.J.	
#journal	J. Biol. Chem. (1989) 264:7092-7095	
#title	Hyperoxic exposure alters gene expression in the lung. Induction of the tissue inhibitor of metalloproteinases mRNA and other mRNAs.	
#cross-references	MUID:89214135	
#accession	A33350	
#molecule_type	mRNA	
##residues	1-206	##label HOR
##cross-references	GB:J04712	
COMMENT	Expression of this protein in the lung is induced 6-fold by hyperoxia.	
CLASSIFICATION	#superfamily metalloproteinase inhibitor	
SUMMARY	#length 206 #molecular-weight 22758 #checksum 4434	
DB 4;	Score 518; Match 40.1%; QryMatch 31.5%; Pred. No. 2.03e-76; Matches 79; Conservative 39; Mismatches 71; Indels 8; Gaps 8;	
Dd	7	lassmlllwlvpactcvpbptafnsdlvirakfvapevnhctt-lyqrveikt 65
Qy	10	LALGILLATLRPADACSPVHPQAFCNADWVRARAKVSEKVDSGNDIYGN-PIKR 68
Dd	66	tk-mkfgfdai-qhatdirfvtvtpamesvcgyshksqnrsseeflagqlr-ngllhhctc 122
Qy	69	IQYEIKQIKMPKGPEKDIEFIYTAPSSAVCGVSLDVGGKKE-YLIAGRAEGDGKMHITLC 127
Dd	123	sfvvpwnslsfqsgfktytaagcdmctvfacasipchlesdhclwtldsalgsd-kgf 181
Qy	128	DFIVPMDTLSTTKQSILNHRVQMCE-CKITRCFMPICYSIPSDDECLMWDWTEKNINGH 186
Dd	182	qsrhiacilpqepglcaw 198
Qy	187	OAKFFACIKRSDGSCAW 203

Search completed: Mon Feb 5 17:00:15 1996  
Job time : 50 secs.

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M P S R H  
\*\*\*\*\*  
(TM)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Mon Feb 5 17:00:33 1996; MasPar time 6.00 Seconds  
Tabular output not generated. 562.012 Million cell updates/sec

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Description: (1:220) from trans.pep  
Perfect Score: 1643  
Sequence: 1 MGAARTLRALGILLATL.....CAWYRGAAPPKQEFLLIEDP 220

Scoring table: PAM 150  
Gap 11

Searched: 43470 seqs, 15335248 residues

Database: swiss-prot31  
1 part1  
2 part2  
3 part3  
4 part4  
5 part5  
6 part6  
7 part7  
8 part8

Statistics: Mean 44.257; Variance 69.417; scale 0.638

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1643	100.0	220	7	TIM2_HUMAN METALLOPROTEINASE INH	0.00e+00
2	1620	98.6	220	7	TIM2_MOUSE METALLOPROTEINASE INH	0.00e+00
3	1550	94.3	220	7	TIM2_BOVIN METALLOPROTEINASE INH	0.00e+00
4	695	42.3	211	7	TIM3_HUMAN METALLOPROTEINASE INH	8.10e-145

5	686	41.8	211	7	TIM3_MOUSE	METALLOPROTEINASE INH	1.77e-142
6	686	41.8	212	7	TIM3_CHICK	METALLOPROTEINASE INH	1.77e-142
7	521	31.7	207	7	TIM1_HUMAN	METALLOPROTEINASE INH	4.90e-100
8	518	31.5	206	7	TIM1_BOVIN	METALLOPROTEINASE INH	2.84e-99
9	517	31.5	207	7	TIM1_MOUSE	METALLOPROTEINASE INH	5.09e-99
10	506	30.8	205	7	TIM1_PIG	METALLOPROTEINASE INH	3.16e-96
11	491	29.9	207	7	TIM1_PIG	METALLOPROTEINASE INH	1.99e-92
12	164	10.0	22	7	TIM2_RAT	METALLOPROTEINASE INH	9.30e-15
13	138	8.4	22	7	TIM1_RAT	METALLOPROTEINASE INH	1.43e-09
14	117	7.1	290	4	HYPB_ECOLI	HYDROGENASE ISOENZYMASE	1.13e-05
15	98	6.0	1025	4	YED7_YEAST	ALPHA-ADAPTIN HOMOLOG	1.85e-02
16	96	5.8	144	8	X62_MOUSE	X62 HEAT STABLE ANTIG	3.84e-02
17	96	5.8	76	4	M163_MOUSE	M1/69-J11D HEAT STABL	3.84e-02
18	93	5.7	404	6	POTG_ECOLI	PUTRESCINE TRANSPORT	1.12e-01
19	91	5.5	206	3	GPBB_HUMAN	PLATELET GLYCOPROTEIN	2.26e-01
20	91	5.5	3033	6	POLG_HCV08	GENOME POLYPROTEIN (C	2.26e-01
21	90	5.5	806	4	ITB7_MOUSE	INTEGRIN BETA-7 SUBUN	3.19e-01
22	89	5.4	1130	4	KABL_HUMAN	PROTO-ONCOGENE TYROSI	4.50e-01
23	89	5.4	1123	4	KABL_MOUSE	PROTO-ONCOGENE TYROSI	4.50e-01
24	88	5.4	80	2	CD24_HUMAN	SIGNAL TRANSDUCER CD2	6.32e-01
25	88	5.4	367	2	DIAC_RAT	DI-N-ACETYLCHITINBIASE	6.32e-01
26	85	5.2	428	5	NODC_RHILP	MODULATION PROTEIN C	1.72e+00
27	84	5.1	1058	6	POL3_DROME	RETROVIRUS-RELATED PO	2.38e+00
28	84	5.1	1042	2	EF3_FNECA	ELONGATION FACTOR 3 (	2.38e+00
29	84	5.1	628	3	GIDA_BACSU	GLUCOSE INHIBITED DIV	2.38e+00
30	83	5.1	267	8	YATR_BACFI	HYPOTHETICAL ATP-BIND	3.28e+00
31	82	5.0	235	1	ATTE_HYACE	PROATTACIN E AND F PR	4.51e+00
32	82	5.0	671	2	COAT_FCVF9	COAT PROTEIN (CAPSID	4.51e+00
33	82	5.0	439	4	KABL_FSVHY	TYROSINE-PROTEIN KINA	4.51e+00
34	82	5.0	1013	6	POL_HUMAN	NAD(+) ADP-RIBOSYLTRA	4.51e+00
35	81	4.9	2116	5	MYX2_DICDI	MYOSIN II HEAVY CHAIN	6.19e+00
36	81	4.9	971	4	MCW3_YEAST	MINICHROMOSOME MAINT	6.19e+00
37	81	4.9	399	2	DNAJ_STRCO	DNAJ PROTEIN.	6.19e+00
38	81	4.9	431	3	HISX_LACIA	HISTIDINOL DEHYDROGEN	6.19e+00
39	81	4.9	3010	6	POLG_HCVTW	GENOME POLYPROTEIN (C	6.19e+00
40	81	4.9	898	6	RA54_YEAST	DNA REPAIR AND RECOMB	6.19e+00
41	80	4.9	619	8	YOL8_CAEEL	HYPOTHETICAL 71.0 KD	8.45e+00
42	80	4.9	544	8	YB73_YEAST	HYPOTHETICAL 62.3 KD	8.45e+00
43	80	4.9	1015	6	PPOL_BOVIN	NAD(+) ADP-RIBOSYLTRA	8.45e+00
44	80	4.9	2265	3	FINC_BOVIN	FIBRONECTIN (FN).	8.45e+00
45	80	4.9	174	3	HDCB_LACS3	20 KD PROTEIN.	8.45e+00

ALIGNMENTS

RESULT	1	TIM2_HUMAN	STANDARD;	PRT;	220 AA.
ID	AC	P16035;			
DT	01-APR-1990	(REL. 14, CREATED)			
DT	01-NOV-1990	(REL. 16, LAST SEQUENCE UPDATE)			
DT	01-FEB-1995	(REL. 31, LAST ANNOTATION UPDATE)			
DE	METALLOPROTEINASE INHIBITOR 2 PRECURSOR (TIMP-2) (TISSUE INHIBITOR OF TIMP2).				
GN	HOMO SAPIENS (HUMAN).				
OS	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; PRIMATES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RM	90338014				



RA STETTLER-STEVENSON W.G., BROWN P.D., ONISTO M., LEVY A.T., LIOTTA L.A.;  
RL J. BIOL. CHEM. 265:13933-13938(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RM 90207285  
RA BOONE T.C., JOHNSON M.J., DE CLERCK Y.A., LANGLEY K.E.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2800-2804(1990).  
RN [3]  
RP SEQUENCE OF 30-214 FROM N.A.  
RA MALIK K., SEJIMA H., AOKI T., IWATA K.;  
RL SUBMITTED (AUG-1990) TO EMBL/GENBANK/DDEJ DATA BANKS.  
RN [4]  
RP SEQUENCE OF 27-219.  
RM 90008902  
RA STETTLER-STEVENSON W.G., KRUTZSCH H.C., LIOTTA L.A.;  
RL J. BIOL. CHEM. 264:17374-17378(1989).  
RN [5]  
RP SEQUENCE OF 30-51; 124-141 AND 159-173.  
RM 90046765  
RA GOLDBERG G.I., MARMER B.L., GRANT G.A., EISEN A.Z., WILHELM S., HE C.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 86:8207-8211(1989).  
RN [6]  
RP SEQUENCE OF 27-41.  
RC TISSUE=SYNOVIAL FLUID;  
RM 92111776  
RA OSTHUES A., KNAUPER V., OBERHOFF R., REINKE H., TSCHESCHE H.;  
RL FEBS LETT. 296:16-20(1992).  
CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)  
CC AND IRREVERSIBLY INACTIVATE THEM.  
CC -1- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF  
CC DISULFIDE BONDS.  
CC -1- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.  
DR EMBL; J05593; HSTIMP2.  
DR EMBL; M32304; HSMET.  
DR EMBL; X54533; HSTIMP2M.  
DR PIR; A34415; A34415.  
DR PIR; A34464; A34464.  
DR PIR; B35996; B35996.  
DR PIR; A37128; A37128.  
DR PIR; S20319; S20319.  
DR MIM; 188825; 11TH EDITION.  
DR PROSITE; PS00288; TIMP.  
KW METALLOPROTEINASE INHIBITOR; SIGNAL.  
FT SIGNAL 1 26  
FT CHAIN 27 220 METALLOPROTEINASE INHIBITOR 2.  
FT DISULFID 27 98 BY SIMILARITY.  
FT DISULFID 29 127 BY SIMILARITY.  
FT DISULFID 39 152 BY SIMILARITY.  
FT DISULFID 134 201 BY SIMILARITY.  
FT DISULFID 172 193 BY SIMILARITY.  
FT DISULFID 159 164 BY SIMILARITY.  
FT CONFLICT 78 78 M -> K (IN REF. 4).  
FT CONFLICT 82 82 P -> I (IN REF. 4).  
FT CONFLICT 96 96 A -> V (IN REF. 3).  
FT CONFLICT 101 101 S -> E (IN REF. 4).  
FT CONFLICT 118 118 MISSING (IN REF. 4).  
FT CONFLICT 122 122 M -> R (IN REF. 4).  
FT CONFLICT 150 150 M -> Q (IN REF. 4).  
FT CONFLICT 175 175 M -> T (IN REF. 4).  
SEQUENCE 220 AA; 24399 MW; 242975 CN;

DB 7; Score 1643; Match 100.0%; OryMatch 100.0%; Pred. No. 0.00e+00;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 mgaartlrlalglalllratllrpdadacscspvhpqqafcnadvvirakavsekevsdnd 60  
QY 1 MGAARTLRLALGLALLLRLATLRLPADAGSCSPVHPQQAFCNADVIRAKAVSEKEVDSND 60  
Db 61 iygnpikriqyeikqikmfkgpekdiefiytapssavcgvslvuggkkeyliagkaegdg 120  
QY 61 IYGNPIKRIQYEI KQIKMFKGPEKDIEFIY TAPSSAVCGVSLDVGGKKEYLIAGKAE G DG 120  
Db 121 kmhitlcdfivpwtlslttgkkslnhryqmgceckitrcpmipcyisspdeciwmwvte 180  
QY 121 KMHITLCDFIVPWTLSLTGKKS LNHR YQMGCECKITRCPMIPCYISSPDECIWMVDWVTE 180  
Db 181 kninghqakffacikrsdgcawyrsgaapkpqefldiedp 220  
QY 181 KNINGHQAKFACIKRSDGSCAWYRSGAAPKPQEFLDIEDP 220  
RESULT 2  
ID TIM2 MOUSE STANDARD; PRT; 220 AA.  
AC P25785;  
DT 01-MAY-1992 (REL. 22, CREATED)  
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
DE METALLOPROTEINASE INHIBITOR 2 PRECURSOR (TIMP-2) (TISSUE INHIBITOR OF  
DE METALLOPROTEINASES-2).  
GN TIMP-2.  
OS MUS MUSCULUS (MOUSE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; RODENTIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
RM 92290292  
RA SHIMIZU S., MALIK K., SEJIMA H., KISHI J.I., HAYAKAWA T., KOIWA O.;  
RL GENE 114:291-292(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RM 92347695  
RA LECO K.J., HAYDEN L.J., SHARMA R.R., ROCHELEAU H., GREENBERG A.H.,  
RA EDWARDS D.R.;  
RL GENE 117:209-217(1992).  
RN [3]  
RP PRELIMINARY SEQUENCE OF 27-62.  
RM 91226375  
RA KISHI J.I., OGAWA K., YAMAMOTO S., HAYAKAWA T.;  
RL MATRIX 11:10-16(1991).  
CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)  
CC AND IRREVERSIBLY INACTIVATE THEM.  
CC -1- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF  
CC DISULFIDE BONDS.  
CC -1- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.  
DR EMBL; X62622; MMTIMP2.  
DR EMBL; M82858; MMTIMP2A.  
DR EMBL; M93954; MMTIMP2B.  
DR PIR; S15987; S15987.  
DR PIR; JH0683; JH0683.

DR PROSITE; PS00288; TIMP.  
KW METALLOPROTEASE INHIBITOR; SIGNAL.  
FT SIGNAL 1 26  
FT CHAIN 27 220  
FT DISULFID 27 98  
FT DISULFID 29 127  
FT DISULFID 39 152  
FT DISULFID 154 201  
FT DISULFID 172 193  
FT DISULFID 159 164  
FT DISULFID 12 12  
FT CONFLICT 21 21  
FT CONFLICT 195 195  
FT CONFLICT 220 AA; 24328 MW; 244289 CN;  
SQ SEQUENCE 220 AA; 24328 MW; 244289 CN;  
DB 7; Score 1620; Match 97.3%; QryMatch 98.6%; Pred. No. 0.00e+00;  
Matches 214; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
Db 1 mgaarelrllalqlllllaelvrpadacscspvhpqafcnadwvirkavsekevdsgnd 60  
Qy 1 MGAARTLRALGLLLATLLRPADACSCSPVHPQAFCNADWVIRAKAVSEKEVDSGND 60  
Db 61 iynpikriqveikqikmfkgpdieftapseaavcgvsldvggkkeyliagkaegdg 120  
Qy 61 IYGNPIKRIQVEIKQIKMFKGPEKDIEFTYAPSSAVCGVSLDVGKKEYLIAGKAEGDG 120  
Db 121 kmhitlcdfivpwtltsitqkkslnhrygmgeckitrcpmipcyisspdeclwmdwvte 180  
Qy 121 KMHITLCDFIVPWTLSITQKKSINHRYQMGCEKITRCMPICYSISPDECLWMDWVTE 180  
Db 181 ksnghqakffacikrdsgeawrgaappkqefldiedp 220  
Qy 181 KNINGHOAKFFACIKRDSGSCAWYRGAAAPPKQEFLDIEDP 220  
RESULT 3  
ID TIM2 BOVIN STANDARD; PRT; 220 AA.  
AC P16368;  
DT 01-AUG-1990 (REL. 15, CREATED)  
DT 01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)  
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
DE METALLOPROTEINASE INHIBITOR 2 PRECURSOR (TIMP-2) (TISSUE INHIBITOR OF  
DE METALLOPROTEINASES-2) (COLLAGENASE INHIBITOR).  
OS BOS TAURUS (BOVINE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; ARTIODACTYLA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RM 90207285  
RA BOONE T.C., JOHNSON M.J., DE CLERCK Y.A., LANGLEY K.E.;  
RL PROC. NATL. ACAD. SCI. U.S.A. 87:2800-2804 (1990).  
RN [2]  
RP SEQUENCE OF 27-71.  
RC TISSUE=CARILAGE;  
RM 86140235  
RA MURRAY J.B., ALLISON K., SUDHALTER J., LANGER R.;  
RL J. BIOL. CHEM. 261:4154-4159 (1986).  
RN [3]  
RP SEQUENCE OF 27-71.  
RM 90008914

RA DE CLERCK Y.A., YEAN T.D., RATZKIN B.J., LU H.S., LANGLEY K.E.;  
RL J. BIOL. CHEM. 264:17445-17453 (1989).  
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)  
CC -!- PTM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF  
CC -!- DISULFIDE BONDS.  
CC -!- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.  
DR EMBL; M32303; BMEET.  
DR PIR; A25322; A25322.  
DR PIR; A35996; A35996.  
DR PIR; A34468; A34468.  
DR PROSITE; PS00288; TIMP.  
KW METALLOPROTEASE INHIBITOR; SIGNAL.  
FT SIGNAL 1 26  
FT CHAIN 27 220  
FT DISULFID 27 98  
FT DISULFID 29 127  
FT DISULFID 39 152  
FT DISULFID 154 201  
FT DISULFID 172 193  
FT DISULFID 159 164  
FT CONFLICT 42 42  
FT CONFLICT 56 56  
FT CONFLICT 68 68  
FT CONFLICT 220 AA; 24355 MW; 234318 CN;  
SQ SEQUENCE 220 AA; 24355 MW; 234318 CN;  
DB 7; Score 1550; Match 91.8%; QryMatch 94.3%; Pred. No. 0.00e+00;  
Matches 202; Conservative 12; Mismatches 6; Indels 0; Gaps 0;  
Db 1 mgaarelrllalqlllllaelvrpadacscspvhpqafcnadwvirkavsekevdsgnd 60  
Qy 1 MGAARTLRALGLLLATLLRPADACSCSPVHPQAFCNADWVIRAKAVSEKEVDSGND 60  
Db 61 iynpikriqveikqikmfkgpdieftapseaavcgvsldvggkkeyliagkaegdg 120  
Qy 61 IYGNPIKRIQVEIKQIKMFKGPEKDIEFTYAPSSAVCGVSLDVGKKEYLIAGKAEGDG 120  
Db 121 nmhitlcdfivpwtltsatqkkslnhrygmgeckitrcpmipcyisspdeclwmdwvte 180  
Qy 121 KMHITLCDFIVPWTLSITQKKSINHRYQMGCEKITRCMPICYSISPDECLWMDWVTE 180  
Db 181 ksnghqakffacikrdsgeawrgaappkqefldiedp 220  
Qy 181 KNINGHOAKFFACIKRDSGSCAWYRGAAAPPKQEFLDIEDP 220  
RESULT 4  
ID TIM3 HUMAN STANDARD; PRT; 211 AA.  
AC P35623;  
DT 01-JUN-1994 (REL. 29, CREATED)  
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)  
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
DE METALLOPROTEINASE INHIBITOR 3 PRECURSOR (TIMP-3) (TISSUE INHIBITOR OF  
DE METALLOPROTEINASES-3).  
GN TIMP3.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.



Db 174 ypqyqkvhacitqkgyswrgwappdkaisnatdp 211  
 Qy 183 INGHQAKFFACIKRSDGSCAWTGAAPKQEFLDIEDP 220

RESULT 6  
 ID TIM3 CHICK STANDARD; PRT; 212 AA.  
 AC P26652;  
 DT 01-AUG-1992 (REL. 23, CREATED)  
 DT 01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
 DE METALLOPROTEINASE INHIBITOR 3 PRECURSOR (TIMP-3) (TISSUE INHIBITOR OF  
 DE METALLOPROTEINASES-3) (21 KD PROTEIN OF EXTRACELLULAR MATRIX).  
 GN IMP-3.  
 OS GALLUS GALLUS (CHICKEN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;  
 OC GALLIFORMES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=EMBRYO FIBROBLAST;  
 RM 92381050  
 RA PAVLOFF N., STASKUS P.W., KISHANANI N.S., HAWKES S.P.;  
 RL J. BIOL. CHEM. 267:17321-17326(1992).  
 RN [2]  
 RP SEQUENCE OF 25-53.  
 RC TISSUE=FIBROBLAST;  
 RM 91093162  
 RA STASKUS P.W., MASIAZ F.R., PALLANCK L.J., HAWKES S.P.;  
 RL J. BIOL. CHEM. 266:449-454(1991).  
 CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)  
 CC AND IRREVERSIBLY INACTIVATE THEM.  
 CC -1- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.  
 DR ENBL; M94531; GGHIMP3A.  
 DR PIR; A39043; A39043.  
 DR PIR; A43429; A43429.  
 DR PROSITE; PS00288; TIMP.  
 KW METALLOPROTEINASE INHIBITOR; SIGNAL.  
 FT SIGNAL 1 24  
 FT CHAIN 25 212 METALLOPROTEINASE INHIBITOR 3.  
 FT DISULFID 25 92 BY SIMILARITY.  
 FT DISULFID 27 119 BY SIMILARITY.  
 FT DISULFID 37 144 BY SIMILARITY.  
 FT DISULFID 146 193 BY SIMILARITY.  
 FT DISULFID 151 156 BY SIMILARITY.  
 FT DISULFID 164 185 BY SIMILARITY.  
 SQ SEQUENCE 212 AA; 24504 MW; 238212 CN;

DB 7; Score 686; Match 45.2%; QryMatch 41.8%; Pred. No. 1.77e-142;  
 Matches 90; Conservative 49; Mismatches 50; Indels 10; Gaps 8;  
 Db 22 aeactcvplhpqdafnsdivirakvvgkllmkdgp--fgt-m-r--ytvqkmkmytqfq 75  
 Qy 24 ADACSSPVPQAFNCADNVIKRAVSEKVEVDSNDIYGNPKIKIQEIKQIKMFKG-P 82  
 Db 76 imphqvviyteaseslcvgklevn-kyqyvitgrvy-egkvytglcnwyekwdrltlsqr 133  
 Qy 83 EK-DIEFIYAPSSAVCGVSLDVGKGKYEYLIAGKAEKGMHITLDFIVPFDLTSTQK 141  
 Db 134 kglhryhlgcgckirpcyylpcfatstneclwtmdlnfghsgtqakhyaciqrvqyc 193  
 :|||||:| | | :|||:| | | | :|||:| | | | :|||:| | | | :|||:| | | |

Qy 142 KSLNRYQMGECKITRCMPICVYISSPDECLMDWVTEKNGHQAFFACIKRSDGSC 201  
 Db 194 awyrgwappdktiinatdp 212  
 Qy 202 AWYRGAAPPKQEFLDIEDP 220

RESULT 7  
 ID TIM1 HUMAN STANDARD; PRT; 207 AA.  
 AC P01033;  
 DT 21-JUL-1986 (REL. 01, CREATED)  
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)  
 DE METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1) (ERYTHROID  
 DE POTENTIATING ACTIVITY) (EPA) (TISSUE INHIBITOR OF METALLOPROTEINASES)  
 DE (FIBROBLAST COLLAGENASE INHIBITOR) (COLLAGENASE INHIBITOR).  
 GN TIMP1 OR TIMP.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RM 86040463  
 RA DOCHERTY A.J.P., LYONS A., SMITH B.J., WRIGHT E.M., STEPHENS P.E.,  
 RA HARRIS T.J.R., MURPHY G., REYNOLDS J.J.;  
 RL NATURE 318:66-69(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RM 85240567  
 RA GASSON J.C., GOLDE D.W., KAUFMAN S.E., WESTBROOK C.A., HEWICK R.M.,  
 RA KAUFMAN R.J., WONG G.G., TEMPLE P.A., LEARY A.C., BROWN E.L.,  
 RA ORR E.C., CLARK S.C.;  
 RL NATURE 315:768-771(1985).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RM 86205964  
 RA CARMICHAEL D.F., SOMMER A., THOMPSON R.C., ANDERSON D.C., SMITH C.G.,  
 RA WELGUS H.G., STRICKLIN G.P.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 83:2407-2411(1986).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA KACZOREK M., HONORE N., RIBES V., DEHOUX P., CORNET P., CARTWRIGHT T.,  
 RA STREECK R.E.;  
 RL BIO/TECHNOLOGY 5:595-598(1987).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RM TISSUE=OVARY;  
 RC 91025550  
 RA RAPP G., FREUDENSTEIN J., KLAUDINY J., MUCHA J., WEMPE F., ZIMMER M.,  
 RA SCHEIT K.H.;  
 RL DNA CELL BIOL. 9:479-485(1990).  
 RN [6]  
 RP DISULFIDE BONDS, AND PARTIAL SEQUENCE.  
 RM 90303199  
 RA WILLIAMSON R.A., MARTON F.A.O., ANGAL S., KOKLITIS P., PANICO M.,  
 RA MORRIS H.R., CAENE A.F., SMITH B.J., HARRIS T.J.R., FREEDMAN R.B.;  
 RL BIOCHEM. J. 268:267-274(1990).  
 RN [7]  
 RP SEQUENCE OF 24-38.  
 RC TISSUE=SYNOVIAL FLUID;

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92111776
RM OSTHUES A., KNAUPER V., OBERHOFF R., REINKE H., TSCHESCHE H.;
RR FEBS LETT. 296:16-20 (1992).
RR [8]
RR MUTAGENESIS.
RM 93041700
R O'SHEA M., WILLENDROCK F., WILLIAMSON R.A., COCKETT M.I.,
RA FREEDMAN R.B., REYNOLDS J.J., DOCHERTY A.J.P., MURPHY G.;
RR BIOCHEMISTRY 31:10146-10152 (1992).
CC -!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC AND IRREVERSIBLY INACTIVATE THEM.
CC -!- FUNCTION: ALSO MEDIATES ERYTHROPOIESIS IN VITRO; BUT, UNLIKE IL-3,
CC IT IS SPECIES-SPECIFIC, STIMULATING THE GROWTH AND DIFFERENTIATION
CC OF ONLY HUMAN AND MURINE ERYTHROID PROGENITORS.
CC -!- PFM: THE ACTIVITY OF TEMP-1 IS DEPENDENT ON THE PRESENCE OF
CC DISULFIDE BONDS.
CC -!- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TEMP FAMILY.
DR EMBL; X03124; HSTIMPR.
DR EMBL; M12670; HSFCI.
DR EMBL; M59906; HSOGCA.
DR EMBL; X56940; HSGR122.
DR PIR; A01269; ZYHOEP.
DR PIR; A23334; A23534.
DR PIR; A35826; A35826.
DR PIR; S20318; S20318.
DR MIM; 305370; 11TH EDITION.
DR PROSITE; PS00288; TEMP.
DR GLYCOPROTEIN; METALLOPROTEASE INHIBITOR; ERYTHROCYTE MATURATION;
KK SIGNAL.
KK 1 23
FT CHAIN 24 207
FT DISULFID 24 93
FT DISULFID 26 122
FT DISULFID 36 147
FT DISULFID 150 197
FT DISULFID 155 160
FT DISULFID 168 189
FT CARBOHYD 53 53
FT CARBOHYD 101 101
FT SEQUENCE 207 AA; 23171 MW; 222441 CN;
SQ DB 7; Score 521; Match 41.1%; QryMatch 31.7%; Pred. No. 4.90e-100
Matches 81; Conservative 39; Mismatches 70; Indels 7; Gaps
Ddb 7 laeqilllllwlapsractcvtppbqtafcnsdlvirakfvgtpevnqtl-lyrveikm 65
Qy 10 LALGILLALLTLIRPADASCSVPHPQQAFQCNADVIRAKAVSEKVDNSGNDIYGN-PIKR 68
Ddb 66 tk-mykqfqaal-qdaadirfvytpamevcgyfhshnrseefllagklq-dgllhittc 122
Qy 69 IQYEIKQIKMFKGPEKDIEFITYAPSSNVCVSLDVGKKKE-YLIAGRAEGDKMHTLC 127
Ddb 123 sfavpwnslalagrfgtktytvccectfpcslsipcqlqsgthclwrdqllqgsekfg 182
Qy 128 DFIVPMDTLSTTQKSLNHRVQMGCE-CKITPCPMIPCISSPDECLMDWVTEKNINGH 186
Ddb 183 qsrhlaclprepqlctw 199
Qy 187 QAKTFACIKRSDGSCAW 203

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RESULT	8
ID	TIML RABIT STANDARD; PRT; 206 AA.
AC	P20614;
AD	01-FEB-1991 (REL. 17, CREATED)
DT	01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
DT	01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DT	01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE	METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1).
DS	ORYCTOLAGUS CINCULIDUS (RABBIT).
ES	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; LAGOMORPHA.
QC	(1)
RN	SEQUENCE FROM N.A.
RP	89214135
RW	HOROWITZ S., DAFNI N., SHAPIRO D.L., HOLM B.A., NOTTER R.H.,
RA	QUIBLE D.J.;
RA	J. BIOL. CHEM. 264:7092-7095(1989).
RL	-!- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
CC	AND IRREVERSIBLY INACTIVATE THEM.
CC	-!- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF
CC	DISULFIDE BONDS.
CC	-!- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.
DR	EMBL; J04712; OSTIMP.
DR	FIR; A33350; A33350.
DR	GROSITE; PS00288; TIMP.
KW	GLYCOPROTEIN; METALLOPROTEINASE INHIBITOR; ERYTHROCYTE MATURATION;
KW	SIGNAL.
FT	CHAIN 1 23
FT	CHAIN 24 206
FT	DLSULFD 24 93
FT	DLSULFD 26 122
FT	DLSULFD 36 147
FT	DLSULFD 150 196
FT	DLSULFD 155 160
FT	DLSULFD 168 188
FT	CARBOHYD 53 53
FT	CARBOHYD 101 101
FT	SEQUENCE 206 AA; 22758 MW; 218998 CN;
DB	7; Score 518; Match 40.1%; QryMatch 31.5%; Pred. No. 2.84e-99-
Matches	79; Conservative 39; Mismatches 71; Indels 8; Gaps 8
Db	7 laasmlllwlvapactcypvhpqtafcnsdlvirakfvgapevnhtt-lydryseikt 65    :      :    :    :    :    :    :    :    :    :    :
Qy	10 LAIGLLLTATLRPADACSCSPVHPQQAFCAVDVIRAKAVSEKVDSGNDIYGN-PIKR 68    :    :    :    :    :    :    :    :    :    :    :
Db	66 tk-mfkfgdal-ghatdriyvftpamesvygshksqrseeefliagqlr-ngllhttc 122 :  :
Qy	69 IQVEIKIQMKFGPEKDIEFIYTAPSAAVCVSLDVDGKKKE-YLIAGKAEGDKMHITLC 127 :  :
Db	123 sfivvpwnslsfqrggfkttyaaagcdmctvfacasipchlesdhclwtadslgsd-kgf 181 :  :
Qy	128 DRIVPWDTLSTTKKSLNHRHYQMGE-KKITRCFMPICYSISPPDECLMDMWVTEKNIGH 186 :  :
Db	182 qarhlaclpqepglcaw 198    :   :   :   :   :   :   :   :   :   :   :   :   :   :
Qy	187 QAQFFACIKRSDGSCAW 203
RESULT	9

[illegible]





Db 1 cscspvhqgafcnadvirak 22  
 QY 27 CSCSPVHPQAFCNADVIRAK 48

RESULT 13  
 ID TIM1 RAT STANDARD; PRT; 22 AA.  
 AC P30120;  
 DT 01-APR-1993 (REL. 25, CREATED)  
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
 DE METALLOPROTEINASE INHIBITOR 1 (TIMP-1) (FRAGMENT).  
 GN TIMP-1.  
 OS RATTUS NORVEGICUS (RAT).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE.  
 RM 92117648

RA ROSWIT W.T., MCCOURT D.W., PARTRIDGE N.C., JEFFREY J.J.;  
 RL ARCH. BIOCHEM. BIOPHYS. 292:402-410(1992).  
 CC -1- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)  
 CC AND IRREVERSIBLY INACTIVATE THEM.  
 CC -1- PTM: THE ACTIVITY OF TIMP-1 IS DEPENDENT ON THE PRESENCE OF  
 CC DISULFIDE BONDS.  
 CC -1- SIMILARITY: HIGH WITH OTHER MEMBERS OF THE TIMP FAMILY.  
 DR PIR; S20326; S20326.  
 DR PROSITE; PS00288; TIMP.  
 KW METALLOPROTEASE INHIBITOR.  
 FT NON TER 22 22  
 SQ SEQUENCE 22 AA; 2363 MW; 2292 CN;

DB 7; Score 136; Match 77.3%; QryMatch 8.4%; Pred. No. 1.43e-09;  
 Matches 17; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 1 cscapthpqtafcnadvirak 22  
 QY 27 CSCSPVHPQAFCNADVIRAK 48

RESULT 14  
 ID HYPB-ECOLI STANDARD; PRT; 290 AA.  
 AC P24190;  
 DT 01-MAR-1992 (REL. 21, CREATED)  
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
 DE HYDROGENASE ISOENZYMES FORMATION PROTEIN HYPB.  
 GN HYPB.  
 OS ESCHERICHIA COLI.  
 OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;  
 OC ENTEROBACTERIACEAE.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RM 91194542

RA LUTZ S., JACOBI A., SCHLENSOG V., BOEHM R., SAVERS G., BOECK A.;  
 RL MOL. MICROBIOL. 5:123-135(1991).  
 CC -1- FUNCTION: IS REQUIRED FOR THE FORMATION OF ALL THREE HYDROGENASE  
 CC ISOENZYMES. AFFECTS SOME ASPECT OF THE PROCESSING OF HYDROGENASES  
 CC 1 AND 2, PERHAPS NICKEL INCORPORATION INTO THE APO-ENZYMES, SINCE  
 CC HYPB GENE LESIONS CAN BE COMPLEMENTED BY HIGH NICKEL ION

CC CONCENTRATION IN THE MEDIUM.  
 CC -1- SIMILARITY: BELONGS TO THE HYPB/HOPM FAMILY.  
 DR EMBL; X54543; ECHYP.  
 DR PIR; S15198; S15198.  
 DR ECO2DBASE; E031.0; 6TH EDITION.  
 DR ECOGENE; E010484; HYPB.  
 KW NICKEL.  
 SQ SEQUENCE 290 AA; 31624 MW; 398662 CN;

DB 4; Score 117; Match 25.2%; QryMatch 7.1%; Pred. No. 1.13e-05;  
 Matches 27; Conservative 27; Mismatches 48; Indels 5; Gaps 5;

Db 120 lltetlmlkdvpcavieggqvtvndaariragtgtgpaigvntgkghida-qmia-daa 177  
 QY 15 LLLATLLPACSCSPVHPQAFCNADVIRAKAVSEKVDGNDIYGNPIKRIQYEIK 74

Db 178 p-rl-plddngilfi-envgnlvcpsafldlgekhkavlavtegedk 221  
 QY 75 QIKMFKGPKDIEFIYTAPSSAVCGVSLDVGGRKEYLIAGKAECDGK 121

RESULT 15  
 ID YB07 YEAST STANDARD; PRT; 1025 AA.  
 AC P38065;  
 DT 01-OCT-1994 (REL. 30, CREATED)  
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)  
 DE ALPHA-ADAPTIN HOMOLOG IN URA7-POL12 INTERGENIC REGION.  
 GN YBLO37W OR YBLO412.  
 OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).  
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C;  
 RA DE WERGIFOSSE P., JACQUES B., JONNIAUX J.L., PURNELLE B., SKALA J.,  
 RA GOFFEAU A.;  
 RL YEAST 10:1489-1496(1994).  
 CC -1- SIMILARITY: STRONG, TO ALPHA ADAPTINS.  
 DR EMBL; X78214; SC22KBF.  
 DR PIR; S42507; SCYBLO37W.  
 KW HYPOTHETICAL PROTEIN; COATED PITS.  
 SQ SEQUENCE 1025 AA; 115011 MW; 5722309 CN;

DB 8; Score 98; Match 29.5%; QryMatch 6.0%; Pred. No. 1.85e-02;  
 Matches 23; Conservative 16; Mismatches 34; Indels 5; Gaps 4;

Db 842 phkraeqsvevskpfdvdespilalnfkcggtstnlnktaigmttttis--sdvnps 899  
 QY 65 PIKRI-Q-YEIKQIMFKGPKDIEFIYTAPSSAVCGVSLDVG-GRKEYLIAGKAECDGK 121

Db 900 mhlmlaqfiskwktlsda 917  
 QY 122 MHITLCDFIVPWTLSIT 139

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